

FIGURE 1: NaIII18 cDNA (SEQ ID NO: 1)

tgaaaagatggcacaggcactgttggtacccccaggacctgaaagcttcgcctttttactaga
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aatgatgactgtacgctcccacggtggcacatgaacgacttcttccactccttccctgattgtgt

FIGURE 1 (continued)

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gagatgggaatggaaccaccagtggtgttaggtactggaagcagtggttgaaaaatacgtaatcga
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FIGURE 1 (continued)

gtaaacaagaggaggtgtctgccgctatcattcagcgtaatttcagatggttatcttttaagca
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gttcctctaccacctctcctccttcctatgatagtgtaacaaaaccagacaaggaaaagtttga
gaaagacaaaccagaaaaagaaagcaaaggaaaagaggtcagagaaaatcaaaagtaaaaagaa
acaaagaattatcttttgatcaattgtttacagcctatga

FIGURE 2: NaIIII18 amino acid (SEQ ID NO: 2)

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDNDDENKPKPNSDLEAG
KNLPFIYGDIPPEMVSEPLEDLDYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVR
KIAIKILVHSLFSMLIMCTILTNCVFM TLSNPPDWTKNVEYTFTGIYTFESLIKILARGF
CLEDFTFRLRDPWNWLD FSVIVMAYVTEFVSLGNVSALRTFRVLRALKTISVIPGLKTIVG
ALIQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGT
MDSNGTFVNVTMSTFNWKDYIGDDSHFYVLDGQKDPLL CGNGSDAGQCPEGYICVKAGRN
PNYGYTSDFTFSWAFSLFRLMTQDYWENLYQLTLRAAGKTYMIFVVLVIFLGSFYLVNL
ILAVVAMAYEEQNQATLEAEQKEAEFQOMLEQLKKQEEAQAVAAASAASRD FSGIGGL
GELLESSEASKLSSKSAKEWRNRKRKRREHLEGNNKGERDSFPKSESEDSVKRSSFL
FSMDGNRLTSDKKFCSPHQSLLSIRGSLFSPPRNSKTSIFSFRGRAKDVGSENFADDEH
STFEDSESRRDSLFVPHRHGERRNSNVSQASMSSRMVPGLPANGKMHSTVDCNGVVS LVG
GPSALTSP TQQLPPEGTTTETEVRKRRLSSYQISM EMLDSSGRQRAVSIASILTNTMEE
LEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDPFVDLAITICIVLNTLFMA
MEHYPMTEQFSSVLT VGNLVFTGIFTAEMVLKIIAMD PYYYFQEGWNI FDGIIVSLSLME
LGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAV
VGMQLFGKSYKECVCKIND DCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQT
MCLIVFMLVMVIGNLVVLNLF LALLSSFS SDNLAATDDDNEMNNLQI AVGRMOKGIDYV
KNKMRECFQKAFFRKPKVIEIHEGNKIDSCMSNNTGIEISKELNYLRDGN GTTSGVGTGS
SVEKYVIDENDYMSFINNPSLT VTPVPIAVGESDFENLNTEEFSSSESELEESKEKLNATSS
SEGSTVDVVLPREGEQAETEPEEDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL RKT
CYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYI FILEMLLK
WVAYGFQTYFTNAWCWLD FLIVDVSLVSLVANALGYSELGAIKSLRTLRLRPLRLSRF
EGMRVVNALVGAI PSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNMTTGNMFDISDV
NNLSDCQALGKQARWKNVKVNF DNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVY
EENLYMYLYFVIFIIFGSFFTLNLF IGVIIDNFNQKKKFGGQDIFMTEEQKKYINAMKK
LGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVTMMVETDDQ GK YMTLVL
SRINLVFIVLFTGEFVLRLVSLRHYYFTIGWNI FDFVVVILSIVGMFLAEMIEKYFVSPT
LFRVIRLARIGRILRLIKGAKGIRTL L FALMMSLPALFNIGLLLFLVMFIYAI FGMSNFA
YVKEAGIDDMFN FETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPDTIHPGSSVK
GDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWE
KFDPDATQFIEFSKLSDFAAALDPPLLI AKPNKVQLIAMDLPMVSGDRIHCLDILFAFTK
RVLGESGEMDALRIQMEDRFMASNPSKVS YEPITTTTLKRKQEEVSAAI IQRNFRCYLLKQ
RLKNISSNYNKEAIKGRIDLP IKQDMIIDKLNGNSTPEKTDGSSSTTSPPSYDSVTKPKDK
EKFEKDKPEKESKGKEVRENQK

**FIGURE 3: cDNA sequence of human SCN3A of Clare et al.
(SEQ ID NO: 3)**

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1  taccctaacc atcttggatg ctgggctttg ttatgctgta attcataagg ctctgtttta
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121 atacctgtca aggattcata gtagagtggc ttactgggaa aggagcaaag aatctcttct
181 agggatattg taagaataaa tgagataatt cacagaaggg acctggagct tttccgaaaa
241 aagggtgctgt gactatctaa ggtaattcgt atgcaagaag ctacacgtaa ttaaagtgtgc
301 aggatgaaaa gatggcacag gcactgttgg tacccccagg acctgaaagc ttccgccttt
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1501 ggaaaacata catgatattt tttgtcctgg tcattttctt gggctcattt tatttgggtga
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1621 aagcagaaca aaaagaggcc gaatttcagc agatgctcga acagcttaaa aagcaacagg
1681 aagaagctca ggcagttgcg gcagcatcag ctgcttcaag agatttcagt ggaatagggtg
1741 ggttaggaga gctgttggaa agttcttcag aagcatcaaa gttgagttcc aaaagtgtca
1801 agaattggag gaaccgaagg aagaaaagaa gacagagaga gcacctgaa ggaaacaaca
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2581 aaatggttct caagatcatt gccatggatc cttattacta tttccaagaa ggctggaata
2641 tctttgatgg aattattgtc agcctcagtt taatggagct tgggtctgtca aatgtggagg
2701 gattgtctgt actgcatcga ttcagactgc tttagttttt caagttggca aaatcctggc
2761 ccacactaaa tatgctaatt aagatcattg gcaattctgt gggggctcta ggaacctca
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2881 agagctacaa agaattgtgtc tgcaagatca atgatgactg tacgctccca cgggtggaca
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3061 tgggtcatgt cattggaaac cttgtggttc tgaacctctt tctggcctta ttgttgagtt
3121 catttagctc agacaacctt gctgctactg atgatgacaa tgaaatgaat aatctgcaga

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FIGURE 3 (continued)

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3241 tccaaaaagc ctttttttaga aagccaaaag ttatagaaat ccatgaaggc aataagatag
3301 acagctgcat gtccaataat actggaattg aaataagcaa agagcttaat tatcttagag
3361 atgggaatgg aaccaccagt ggtgtaggta ctggaagcag tggtgaaaaa tacgtaatcg
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3541 tagaagaaag caaagagaaa tttaatgcaa ccagctcatc tgaaggaagc acagttgatg
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5101 ttgctttgat gatgtccctt cctgcgttgt ttaacatcgg cctcctgctc ttcttggtca
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5941 actataacaa agaggcaatt aaaggaggga ttgacttacc tataaaacaa gacatgatta
6001 ttgacaaact aaatgggaac tccactccag aaaaaacaga tgggagttcc tctaccacct
6061 ctctctcttc ctatgatagt gtaacaaaac cagacaagga aaagtttgag aaagacaaac
6121 cagaaaaaga aagcaaagga aaagaggtca gagaaaatca aaagtaaaaa gaacaaaaga
6181 attatctttg tgatcaattg tttacagcct atgaaggtaa agtatatgtg tcaactggac
6241 ttcaagagga ggtccatgcc aaactgactg ttttaacaaa tactcatagt cagtgcctat
6301 acaagacagt gaagtgcct ctctgtcact gcaactctgt gaagcagggt atcaacattg
6361 acaagaggtt gctgttttta ttaccagctg acactgctga ggagaaaccc aatggctacc

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FIGURE 3 (continued)

6421 tagactatag ggatagttgt gcaaagtga cattgtaact acaccaaaca ctttagtac
6481 agtccttgca tccattctat ttttaacttc catatctgcc atatttttac aaaatttggt
6541 ctagtgcatt tccatgggcc ccaattcata gtttattcat aatgctatgt cactatattt

FIGURE 4: amino acid sequence of human SCN3A (SEQ ID NO: 4)

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDNDNENKPKPNSDLEAGKNLPFI
YGDIPPEMVSEPLEDLDPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKIAIKILVHS
LFSMLIMCTILTNCVFM TLSNPPDWTKNVEYFTFTGIYTFESLIKILARGEFCLEDFTF LRDPWNW
LDFSVIVMAYVTEFVSLGNVSALRTFRVLRLAKTISVIPGLKTI VGALIQSVKKLS DVMILT VF
CLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFN GTMDSNGTFVNV TMSTFNWKDYIG
DDSHFYVLDGQKDPLL CGNGSDAGQCPEGYI CVKAGRNP NYGYTSFD TFSWAFLSL FRLMTQDY
WENLYQLTLRAAGKTYMIF FVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEA EQKEAEFQQM
LEQLKKQQEEAQAVAAASAASRDFSGIGGLGELLE SSEASKLSSKSAKEWRNRKRKRQREHL
EGNNKGERDSFPKSESEDSVKRSSFLFSMDGNRLTSDKKFCSPHQSLLSIRGSLFS PRNRNSKTS
IFSFRGRAKDVGSENDFADDEHSTFEDSESRD SLFVPHRHGERRNSNGTTTETEVRKRRLSSY
QISMEMLEDSSGRQRAVSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLV
NLIVMDPPFDLAI TICIVLNTLFMAMEHYPMTEQFSSVLT VGNLVFTGIFTAEMVLKIIAMDPY
YYFQEGWNIFDGIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGA
LGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKIND DCTLPRWHMNDFFHSFLIVFRVLCGEWI
ETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLNLF LALLLSSFS SDNLAATDDD NEMNNLQI AVG
RMQKGIDYVKNKMREC FQKAFFRKPKVIEIHEGNKIDSCMSNNTGIEISKELNYLRDGN GTTSG
VGTGSSVEKYVIDENDYMSFINNPSLTVTVP IAVGESDFENLNTEEFSSSESELEESKEKLNATS
SSEGSTVDVVLPREGEQAETEPEEDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYS
IVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWWAYGFQ
TYFTNAWCWLD FLIVDVSLVSLVANALGYSELGA IKSRLTLRALRPLRALS RFEGMRVVVNALV
GAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNM TTGNMFDI SDVNNLSDCQALGKQARW
KNVKVNF DNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEE NLYMYLYFVIFIFGSF
FTLNLFIGVIIDNFNQKKKFGQDIFMTEEQKKY NAMYKLGSKKPQKPIPRPANKFQGMVFD
FVTRQVFDISIMILICLNMVTMMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYF
TIGWNIFDFVVVILSIVGMFLAEMIEKYFVSPTLFRVIRLARIGRI LRLIKGAKGIRTLLFALM
MSLPALFNIGLLLFLVMFIY AIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDG
LLAPILNSAPPD CDPD TIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVA
TEESAEP LSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAALDPPLLI AKPNKVQLIAMDLPM
VSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEDRFMASNPSKVS YEPI TTTLKRKQEEVSAA
IIQRNFR CYLLKQRLKNISSNYNKEAIKGRIDLP IKQDMIIDKLNGNSTPEKTDGSSSTTSPPS
YDSVTKPDKEKF EKDKPEKESKGKEVRENQK

FIGURE 5: cDNA of human sodium channel α -subunit variant by Jeong et al. (SEQ ID NO: 5)

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1 agcgaagcgg aggcataagc agagaggatt ctggaaaggt ctctttgttt tcttatccac
61 agagaaagaa agaaaaaaaa ttgtaactaa tttgtaaacc tctgtggtca aaaaaaaaaa
121 aaaaaaaaaa gctgaacagc tgccagagga agacacgtta taccctaacc atcttggtg
181 ctgggctttg ttatgctgta attcataagg ctctgtttta tcagagatta tggagcaaga
241 aaactgaagc caagccacat caagggttga cagggatgag atacctgtca aggattcata
301 gtagagtggc ttactgggaa aggagcaaag aatctcttct agggatattg taagaataaa
361 tgagataatt cacagaaggg acctggagct tttccggaaa aagggtgctgt gactatctaa
421 ggtaattcgt atgcaagaag ctacacgtaa ttaaatgtgc aggatgaaaa gatggcacag
481 gcactgttgg tacccccagg acctgaaagc ttccgccttt ttactagaga atctcttgct
541 gctatcgaaa aacgtgctgc agaagagaaa gccaaagaagc ccaaaaagga acaagataat
601 gatgatgaga acaaaccaaa gccaaatagt gacttggaag ctggaaagaa ccttcattt
661 atttatggag acattcctcc agagatgggt tcagagcccc tggaggacct ggatccctac
721 tatatcaata agaaaacttt tatagtaatg aataaaggaa aggcaatttt ccgattcagt
781 gccacctctg ccttgatat tttactcca ctaaaccctg ttaggaaaat tgctatcaag
841 attttggtag attctttatt cagcatgctt atcatgtgca ctattttgac caactgtgta
901 tttatgacct tgagcaaccc tctgactgg acaaagaatg tagagtacac attcactgga
961 atctatacct ttgagtcact tataaaaatc ttggcaagag ggttttgctt agaagatttt
1021 acgtttcttc gtgatccatg gaactggctg gatttcagt tcatgtgat ggcataatgt
1081 acagagtttg tggacctggg caatgtctca gcgttgagaa cattcagagt tctccgagca
1141 ctgaaaacaa tttcagtcac tccaggttta aagaccattg tgggggcccc gatccagtcg
1201 gtaaaagcgc tttctgatgt gatgatcctg actgtgttct gtctgagcgt gtttgcctc
1261 attgggctgc agctgttcat gggcaatctg aggaataaat gtttgagtg gcccccagc
1321 gattctgctt ttgaaaccaa caccacttcc tactttaatg gcacaatgga ttcaaaggg
1381 acatttggtt atgtaacaat gagcacattt aactggaagg attacattgg agatgacagt
1441 cacttttatg ttttgatgg gcaaaaagac cttttactct gtggaaatgg ctcatgtgca
1501 ggccagtgct cagaaggata catctgtgtg aaggctgggtc gaaaccccaa ctatggctac
1561 acaagctttg acacctttag ctgggctttc ctgtctctat ttogactcat gactcaagac
1621 tattgggaaa atctttacca gttgacatta cgtgctgctg ggaaaacata catgatattt
1681 tttgtcctgg tcattttctt gggctcattt tatttgggtg atttgatcct ggctgtggtg
1741 gccatggcct atgaggagca gaatcaggcc accttggaag aagcagaaca aaaagaggcc
1801 gaatttcagc agatgctcga acagcttaaa aagcaacagg aagaagctca ggcagttgctg
1861 gcagcatcag ctgcttcaag agatttcagt ggagtaggtg ggttaggaga gctgttgga
1921 agttcttcag aagcatcaaa gttgagttcc aaaggtgcta aagaatggag gaaccggagg
1981 aagaaaagaa gacagagaga gcacctgaa ggaaacaaca aaggagagag agacagcttt
2041 cccaaatccg aatctgaaga cagcgtcaaa agaagcagct tccttttctc catggatgga
2101 aacagactga ccagtgaaca aaaattctgc tccctcatc agtctctctt gagtatccgt
2161 ggctccctgt tttcccagc acgcaatagc aaaacaagca ttttcagttt cagaggtcgg
2221 gcaaaggatg ttggatctga aaatgacttt gctgatgatg aacacagcac atttgaagac
2281 ggcgaaagca ggagagactc actgtttgtg ccgcacagac atggagagcg acgcaacagt
2341 aacgttagtc aggccagtat gtcattccagg atgggtgccag ggcttccagc aaatgggaag
2401 atgcacagca ctgtggattg caatggtgtg gtttccttgg tgggtggacc ttcagctcta
2461 acgtcaccta ctggacaact tccccagag ggcaccacca ctgaaacgga agtcagaaag
2521 agaaggttaa gctcttacca gatttcaatg gagatgctgg aggattcctc tggaaaggcaa
2581 agagccgtga gcatagccag cattctgacc aacacaatgg aagaacttga agaacttaga
2641 cagaaatgtc cgccatgctg gtatagattt gccaatgtgt tcttgatctg ggactgctgt
2701 gatgcatggt taaaagtaaa acatcttctg aatttaattg ttatggatcc atttgttgat
2761 ctgtgccatca ctatttgcac tgtcttaaat acctcttta tggccatgga gcactacccc
2821 attgtagcagc aattcagtag tgtgttgact gtaggaaacc tggctcttac tgggattttc
2881 acagcagaaa tggttctcaa gatcattgcc atggatcctt attactattt ccaagaaggc
2941 tgggaatatct ttgatggaat tattgtcagc ctcatgttaa tggagcttgg tctgtcaaat
3001 gtggagggat tgtctgtact gcgatcattc agactgctta gagttttcaa gttggcaaaa
3061 tcctggccca cactaaatat gctaattaag atcattggca attctgtggg ggccttagga
3121 aacctcacct tgggtgttggc catcatcgct ttcatttttg ctgtggctcg catgcagctc

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FIGURE 5 (continued)

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3181 tttggtgaaga gctacaaaga atgtgtctgc aagatcaatg atgactgtac gctccacgg
3241 tggcacatga acgacttctt ccactccttc ctgatttgtt tccgcgtgct gtgtggagag
3301 tggatagaga ccatgtggga ctgtatggag gtcgctggcc aaaccatgtg ccttattgtt
3361 ttcattgttg tcatggtcat tggaaacctt gtggttctga acctctttct ggccttatta
3421 ttgagttcat ttagctcaga caaccttgct gctactgatg atgacaatga aatgaataat
3481 ctgcagattg cagtaggaag aatgcaaaag ggaattgatt atgtgaaaaa taagatgagg
3541 gagtgtttcc aaaaagcctt ttttagaaag ccaaaagtta tagaaatcca tgaaggcaat
3601 aagatagaca gctgcatgtc caataatact ggaattgaaa taagcaaaga gcttaattat
3661 cttagagatg ggaatggaac caccagtggg ttaggtactg gaagcagtgt tgaaaaatac
3721 gtaatcgatg aaaatgatta tatgtcattc ataaacaacc ccagcctcac cgtcacagt
3781 ccaattgctg ttggagagtc tgactttgaa aacttaataa ctgaagagtt cagcagtgtg
3841 tcagaactag aagaaagcaa agagaaatta aatgcaacca gctcatctga aggaagcaca
3901 gttgatgttg ttctaccccg agaaggtgaa caagctgaaa ctgaaccoga agaagacttt
3961 aaaccggaag cttgttttac tgaaggggtg attaaaaagt ttccattctg tcaagtaagt
4021 acagaagaag gcaaagggaa gatctgggtg aatcttcgaa aaacctgcta cagtattgtt
4081 gagcacaact ggtttgagac tttcattgtg ttcattgatc ttctcagtag tgggtcattg
4141 gcctttgaag atatatacat tgaacagcga aagactatca aaaccatgct agaattatgt
4201 gacaaagtct ttacctatat attcattctg gaaatgcttc tcaaatgggt tgcttatgga
4261 tttcaaacat atttactata tgccctgtgc tggctagatt tcttgatcgt tgatgtttct
4321 ttggttagcc tggtagccaa tgctcttggc tactcagaac tcggtgccat caaatcatta
4381 cggacattaa gagctttaag acctctaaga gccttatccc ggtttgaagg catgaggggtg
4441 gttgtgaatg ctcttggttg agcaattccc tctatcatga atgtgctgtt ggtctgtctc
4501 atcttctggg tgatctttag catcatgggt gtgaatttgt ttgctggcaa gttctaccac
4561 tgtgttaaca tgacaacggg taacatgttt gacattagtg atgttaacaa tttgagtgtc
4621 tgtcaggctc ttggcaagca agctcggtgg aaaaacgtga aagtaaactt tgataatgtt
4681 ggcgctggct atcttgcaat gcttcaagtg gccacattta aaggctggat ggatattatg
4741 tatgcagctg ttgattcacg agatgttaaa ctctagcctg tatatgaaga aaatctgtac
4801 atgtatttat actttgtcat ctttatcatc tttgggtcat tcttctactc gaatctattc
4861 attggtgtca tcatagataa cttcaaccag cagaaaaaga agtttggagg tcaagacatc
4921 tttatgacag aggaacagaa aaaatattac aatgcaatga agaaacttgg atccaagaaa
4981 cctcagaaac ccatacctcg ccagcaaac aaattccaag gaatggctct tgattttgta
5041 accagacaag tctttgatat cagcatcatg atcctcatct gcctcaacat ggtcaccatg
5101 atggtggaag cggatgacca gggcaaatat atgaccctag ttttgtcccg gatcaacctt
5161 gtgttcattg ttctgttcac tggagaattt gtgctgaagc tcgtttccct cagacactac
5221 tacttacta taggctggaa catctttgac tttgtggtgg tgattctctc caattgtagt
5281 atgtttctgg ctgagatgat agaaaagtat tctgtgtccc ctacctgtt cggatgtatc
5341 cgtcttgcca ggattggccg aatcctacgt ctgatcaaag gagcaaaggg gatccgcacg
5401 ctgctctttg ctttgatgat gtcccttctc gcgttggtta acatcggcct cctgctcttc
5461 ctggtcatgt ttatctatgc catctttggg atgtccaact ttgcctatgt taaaaaggaa
5521 gctggaattg atgacatgtt caactttgag acctttggca acagcatgat ctgcttgttc
5581 caaattacaa cctctgctgg ctgggatgga ttgctagcac ctattcttaa tagtgacca
5641 cccgactgtg accctgacac aattcacctt ggcagctcag ttaagggaga ccgtggggac
5701 ccactctgtg ggattttctt ttttgtcagt tacatcatca tatccttctt ggttgtgtgtg
5761 aacatgtaca tcgcggtcat cctggagaac ttcagtgttg ctactgaaga aagtgcagag
5821 cccctgagtg aggatgactt tgagatgttc tatgaggttt gggaaaagt tgaatccgat
5881 ccgacccagt ttatagagtt ctctaaactc tctgattttg cagctgccct ggatcctcct
5941 cttctcatag caaaacccaa caaagtccag cttattgcca tggatctgcc catggtcagt
6001 ggtgaccgga tccactgtct tgatatttta tttgccttta caaagcgtgt tttgtgtgag
6061 agtggagaga tggatgccct tcgaatacag atggaagaca ggtttatggc atcaaacccc
6121 tccaaagtct cttatgagcc tattacaacc actttgaaac gtaaacaaaga ggaggtgtct
6181 gccgctatca ttcagcgtaa tttcagatgt tatcttttaa agcaaagggt aaaaaatata
6241 tcaagtaact ataacaaaga ggcaattaaa gggaggattg acttacctat aaaaagagac
6301 atgattattg acaaaactaa tgggaactcc actccagaaa aaacagatgg ggttcctct
6361 accaccctc ctccttctta tgatagtgtg acaaaaaccag acaaggaaaa gtttgagaaa

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FIGURE 5 (continued)

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6421 gacaaaccag aaaaagaaag caaaggaaaa gaggtcagag aaaatcaaaa gtaaaaagaa
6481 acaaagaatt atctttgtga tcaattgttt acagcctatg aaggtaaagt atatgtgtca
6541 actggacttc aagaggaggt ccatgccaaa ctgactgttt taacaaatac tcatagtcag
6601 tgcctataca agacagtga gtagaccttc tgtcactgca actctgtgaa gcagggtatc
6661 aacgttgaca agaggttgct gtttttatta ccagctgaca ctgctgagga gaaacccaat
6721 ggctacctag actataggga tagttgtgca aagtgaacat tgtaactaca ccaaacacct
6781 ttagtacagt ccttgcatcc attctatttt taacttccat atctgccata tttttacaaa
6841 atttgttcta gtgcatttcc atgggtccca attcatagtt tattcataat gctatgtcac
6901 tatttttgta aatgaggttt acggtgaaga aacagtatac aagaaccctg tctctcaaat
6961 gatcagacaa aggtgttttg ccagagagat aaaatttttg ctcaaaacca gaaaaagaat
7021 tgtaatggct acagtttcag ttacttccat tttctagatg gctttaattt tgaaagtatt
7081 ttagtctgtt atgtttgttt ctatctgaac agttatgtgc ctgtaaagtc tcctctaata
7141 tttaaaggat ttttttatg caaagtattc tgtttcagca agtgcaaat ttattctaag
7201 tttcagagct ctatatttaa tttaggtcaa atgctttcca aaaagtaatc taataaatcc
7261 attctagaaa aatatactta aagtattgct ttagaatagt tgttccactt tctgctgcag
7321 tattgctttg ccatctcttg ctctcagcaa agctgatagt ctatgtcaat taaataccct
7381 atgttatgta aatagttatt ttatcctgtg gtgcatgttt gggcaaatat atatatagcc
7441 tgataaacaa ctctatttaa atcaaatatg taccacagtg tatgtgtctt ttgcaagctt
7501 ccaacagggg tgtatcctgt atcattcatt aaacatagtt taaaggctat cactaatgca
7561 tgttaatat ttgcctatgct ctctatttta ctcaatccat tcttcacaag tcttggttaa
7621 agaatgtcac atattggtga tagaatgaat tcaacctgct ctgtccatta tgtcaagcag
7681 aataatttga agctattttac aaacaccttt acttttgcac ttttaattca acatgagtat
7741 catatggtat ctctctggat ttcaaggaaa cacactggat actgcctact gacaaaacct
7801 attcttcata ttttgctaaa aatatgtcta aaacttgttt aaatataaat aatgtaaaaa
7861 tataatcaac tttatttgtc agcattttgt acataagaaa attattttca ggttgatgac
7921 atcacaattt attttacttt atgcttttgc ttttgatttt taatcacaat tccaaacttt
7981 tgaatccata agatttttca atggataatt tcttaaaata aaagttagat aatgggtttt
8041 atggatttct ttgttataat atattttcta ccattccaat aggagatata ttgggtcaaac
8101 actcaaacct agatcatttt ctaccaacta tgggtgcctc aatataacct tttattcata
8161 gatgtttttt tttattcaac ttttgtagta ttacgtatg cagactagtc ttattttttt
8221 aattcctgct gcactaaagc tattacaaat ataacatgga ctttgttctt tttagccatg
8281 aacaaagtgg caaagtgttg caattacctt acatgatata aatttttgtt ttttgcaaaa
8341 accaaaagtt taatgttaat tctttttaca aaactattta ctgtagtgta ttgaagaact
8401 gcatgcaggg aattgctatt gctaaaaaga atgggtgagct acgtcattat tgagccaaaa
8461 gaataaattt cattttttat tgcatttcac ttattgggct ctgggggttt ttgtttttgt
8521 tttttgctgt tggcagttta aaatatatat aattaataaa acctgtgctt gatctgacat
8581 ttgtatacat aaaagtttac atgaatttta caacaaacta gtgcatgatt caccaagcag
8641 tactacagaa caaaggcaaa ttaaaagcag ctttgtgaac ttttatgtgt gcaaaggatc
8701 aagttcacat gttccaactt tcagggttga taataatagt agtaaccacc tacaatagct
8761 ttcaatttca attaaactcc ttggctataa gcattctaac tcatcttctt tcaatataat
8821 tgatgctatc tcttaattac ttgggtggcta ataaatgtta cattctttgt tacttaaatg
8881 cattatataa actcctatgt atacataagg tattaatgat atagttattg agaatttata
8941 ttaacttttt tttcaagaac ctttgatttt atgtgaggtc aaaaccaaac tcttattctc
9001 agtggaaaaa tccagttgta atgcatattt ttaaagacaa tttggatcta aatatgtatt
9061 tcataattct ccataataa attatataag gtggaaaaaa aaaaaaaaaa aaaaaaaaaa
9121 aaa

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FIGURE 6: amino acid sequence of human sodium channel α -subunit variant by Jeong et al. (SEQ ID NO: 6)

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDNDDENKPKPNSDLEAGKNLPFI
YGDIPPEMVSEPLEDLDPPYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKIAIKILVHS
LFSMLIMCTILTNCVFM TLSNPPDWTKNVEYTF TGIYTFESLIKILARGFCLEDFTFLRDPWNW
LDFSVIVMAYVTEFVDLGNVSALRTFRVL RALKTISVIPGLKTIVGALIQSVKKLS DVMILTVF
CLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGTMD SNGTFVNVTMSTFNWKDYIG
DDSHFYVLDGQKDP LLCNGSGDAGQCPEGYICVKAGRNP NYGYTSFDTF SWAFLSLFR LMTQDY
WENLYQLTLRAAGKTYMIF FVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEA EQKEAEFQQM
LEQLKKQEEAQAVAAASAASRDFSGVGGLGELLESSEASKLSSKGAK EWRNRKRQRREHL
EGNNKGERDSFPKSESEDSVKRSSFLFSMDGNRLTSDKKFCSPHQSLLSIRGSLFS PRNSKTS
IFSFRGRAKDVGSENDFADDEHSTFEDGE SRRDSL FVPHRHGERRNSNVSQASMSSRMV PGLPA
NGKMHSTVDCNGVVS LVGGPSALTSP TGQLPPEGTTTETEVKRRLSSYQI SMEMLEDSSGRQR
AVSIA SILTNTMEELEESRQKCP PCWYRFANVFLIWDCCDAWLKV KHLVNLIVMDP FVDLAI TI
CIVLNTLFMAMEHYPMTEQFSSVLT VGNLVFTGIFTAEMVLKI IAMPY YFFQEGWNIFDGIIV
SLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKI IGNSVGALGNLTLVLAIIVFIF
AVVGMQLFGKSYKECVCKIND DCTLPRWHMNDFFH SFLIVFRVLCGEW IETMWDCMEVAGQ TMC
LIVFMLVMVIGNLVVLNLF LALLSSFS SDNLAATDDD NEMNNLQI AVGRMQKGIDYVKNMRE
CFQKAFFRKPKVIEIHEGNKIDSCMSNNTGIEISKELNYLRDGN GTTSGVGTGSSVEKYVIDEN
DYMSFINNP SLTVTVPIAVGESDFENL NTEEFSSSESELEESKEKLNATSS SEGSTVDVVL PREG
EQAETEPEEDFKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL RKTCYSIVEHNWFET FIVFMI
LLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYI FILEMLLKWVAYGFQTYFTNAWCWLD FLIV
DVSLVSLVANALGYSELGA IKSRLTLRALRPLRALS RFEGMRVVVNALVGA IPSIMNVLLVCLI
FWLIFSIMGVNLFAGKFYHCVNM TTNMFDISDVNNLSDCQALGKQARWKNVKNF DNVGAGYL
ALLQVATFKGWMDIMYAAVDSRDVKLQPVYEE NLYMYLYFVIFII FGSFFTLNLF IGVIIDNFN
QQKKKFGGQDIFMTEE QKKYINAMKKLGSKKPQKPI PRPANKFQGMV FDFVTRQVFDISIMILI
CLNMVTMMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNI FDFVVVILS
IVGMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIR TLLFALMMSLPALFNIGLLLFL
VMFIYAI FGMSNFAYVKKEAGIDDMFN FETFGNSMICLFQITTSAGWDGL LAPILNSAPPDCDP
DTIHPGSSSVKGDRGDPSVGIFFFVS YIIISFLVVVNMYIAVILENFSVATEESA EPLSEDDFEM
FYEVWEKFDPDATQFIEFSKLSDFAAALDPPLLI AKPNKVQLIAMDLPMVSGDRIHCLDILFAF
TKRVLCESGEMDALRIQMEDRFMASNPSKVS YEPITTTLKRKQEEVSAAI IQRNFR CYLLKQRL
KNISSYNKEAIKGRIDLPIKQDMIIDKLNGNSTPEKTDGSSSTTPPPSYDSVTKPDKEKFEKD
KPEKESKGKEVRENQK

		Section 1						
		(1)	1	10	20	30	48	
ClareAJ251507	(1)	-----						
huNall18 (AK)	(1)	-----						
JeongAF225987	(1)	AGCGAAGCGGAGGCATAAGCAGAGAGGATTCTGGAAAGGTCTCTTTGT						
Consensus	(1)							
		Section 2						
		(49)	49	60	70	80	96	
ClareAJ251507	(1)	-----						
huNall18 (AK)	(1)	-----						
JeongAF225987	(49)	TTTCTTATCCACAGAGAAAGAAAGAAAAAAATTGTAACATAATTGTA						
Consensus	(49)							
		Section 3						
		(97)	97	110	120	130	144	
ClareAJ251507	(1)	-----						
huNall18 (AK)	(1)	-----						
JeongAF225987	(97)	AACCTCTGTGGTCAAAAAAAAAAAAAAAAAAGCTGAACAGCTGCC						
Consensus	(97)							
		Section 4						
		(145)	145	150	160	170	180	192
ClareAJ251507	(1)	TACCGTAACCATCTTGGATGCTGGGCTTTGTT						
huNall18 (AK)	(1)	TACCGTAACCATCTTGGATGCTGGGCTTTGTT						
JeongAF225987	(145)	AGAGGAAGACACGTTATACCGTAACCATCTTGGATGCTGGGCTTTGTT						
Consensus	(145)	TACCGTAACCATCTTGGATGCTGGGCTTTGTT						
		Section 5						
		(193)	193	200	210	220	230	240
ClareAJ251507	(33)	ATGCTGTAATTTCATAAGGCTCTGTTTATCAGAGATTATGGAGCAAGA						
huNall18 (AK)	(1)	ATGCTGTAATTTCATAAGGCTCTGTTTATCAGAGATTATGGAGCAAGA						
JeongAF225987	(193)	ATGCTGTAATTTCATAAGGCTCTGTTTATCAGAGATTATGGAGCAAGA						
Consensus	(193)	ATGCTGTAATTTCATAAGGCTCTGTTTATCAGAGATTATGGAGCAAGA						
		Section 6						
		(241)	241	250	260	270	288	
ClareAJ251507	(81)	AAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAGATACCTGT						
huNall18 (AK)	(1)	AAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAGATACCTGT						
JeongAF225987	(241)	AAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAGATACCTGT						
Consensus	(241)	AAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAGATACCTGT						
		Section 7						
		(289)	289	300	310	320	336	
ClareAJ251507	(129)	CAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAGAATCTC						
huNall18 (AK)	(1)	CAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAGAATCTC						
JeongAF225987	(289)	CAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAGAATCTC						
Consensus	(289)	CAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAGAATCTC						

Section 8							
	(337)	337	350	360	370	384	
ClareAJ251507	(177)	TTCTAGGGATATTGTAAGAATAAATGAGATAATTCACAGAAGGGACCT					
huNall18 (AK)	(1)	-----					
JeongAF225987	(337)	TTCTAGGGATATTGTAAGAATAAATGAGATAATTCACAGAAGGGACCT					
Consensus	(337)	TTCTAGGGATATTGTAAGAATAAATGAGATAATTCACAGAAGGGACCT					
Section 9							
	(385)	385	390	400	410	420	432
ClareAJ251507	(225)	GGAGCTTTTCCGGAAAAAGGTGCTGTGACTATCTAAGGTAATTCGTAT					
huNall18 (AK)	(1)	-----					
JeongAF225987	(385)	GGAGCTTTTCCGGAAAAAGGTGCTGTGACTATCTAAGGTAATTCGTAT					
Consensus	(385)	GGAGCTTTTCCGGAAAAAGGTGCTGTGACTATCTAAGGTAATTCGTAT					
Section 10							
	(433)	433	440	450	460	470	480
ClareAJ251507	(273)	GCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAG					
huNall18 (AK)	(1)	-----TGAAAAGATGGCACAG					
JeongAF225987	(433)	GCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAG					
Consensus	(433)	GCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAG					
Section 11							
	(481)	481	490	500	510	528	
ClareAJ251507	(321)	GCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTACTAGA					
huNall18 (AK)	(17)	GCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTACTAGA					
JeongAF225987	(481)	GCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTACTAGA					
Consensus	(481)	GCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTACTAGA					
Section 12							
	(529)	529	540	550	560	576	
ClareAJ251507	(369)	GAATCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAG					
huNall18 (AK)	(65)	GAATCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAG					
JeongAF225987	(529)	GAATCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAG					
Consensus	(529)	GAATCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAG					
Section 13							
	(577)	577	590	600	610	624	
ClareAJ251507	(417)	AAGCCCCAAAAGGAACAAGATAATGATGATGAGAACAACCAAAGCCA					
huNall18 (AK)	(113)	AAGCCCCAAAAGGAACAAGATAATGATGATGAGAACAACCAAAGCCA					
JeongAF225987	(577)	AAGCCCCAAAAGGAACAAGATAATGATGATGAGAACAACCAAAGCCA					
Consensus	(577)	AAGCCCCAAAAGGAACAAGATAATGATGATGAGAACAACCAAAGCCA					
Section 14							
	(625)	625	630	640	650	660	672
ClareAJ251507	(465)	AATAGTGACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGAC					
huNall18 (AK)	(161)	AATAGTGACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGAC					
JeongAF225987	(625)	AATAGTGACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGAC					
Consensus	(625)	AATAGTGACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGAC					

Section 15						
	(673)	673	680	690	700	710 720
ClareAJ251507	(513)	ATTCTCCAGAGATGGTGTCTCAGAGCCCCTGGAGGACCTGGATCCCTAC				
huNall18 (AK)	(209)	ATTCTCCAGAGATGGTGTCTCAGAGCCCCTGGAGGACCTGGATCCCTAC				
JeongAF225987	(673)	ATTCTCCAGAGATGGTGTCTCAGAGCCCCTGGAGGACCTGGATCCCTAC				
Consensus	(673)	ATTCTCCAGAGATGGTGTCTCAGAGCCCCTGGAGGACCTGGATCCCTAC				
Section 16						
	(721)	721	730	740	750	768
ClareAJ251507	(561)	TATATCAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGGCAATT				
huNall18 (AK)	(257)	TATATCAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGGCAATT				
JeongAF225987	(721)	TATATCAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGGCAATT				
Consensus	(721)	TATATCAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGGCAATT				
Section 17						
	(769)	769	780	790	800	816
ClareAJ251507	(609)	TTCCGATTTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAAC				
huNall18 (AK)	(305)	TTCCGATTTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAAC				
JeongAF225987	(769)	TTCCGATTTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAAC				
Consensus	(769)	TTCCGATTTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAAC				
Section 18						
	(817)	817	830	840	850	864
ClareAJ251507	(657)	CCTGTTAGGAAAATTGCTATCAAGATTTTGGTACATTCTTTATTTCAGC				
huNall18 (AK)	(353)	CCTGTTAGGAAAATTGCTATCAAGATTTTGGTACATTCTTTATTTCAGC				
JeongAF225987	(817)	CCTGTTAGGAAAATTGCTATCAAGATTTTGGTACATTCTTTATTTCAGC				
Consensus	(817)	CCTGTTAGGAAAATTGCTATCAAGATTTTGGTACATTCTTTATTTCAGC				
Section 19						
	(865)	865	870	880	890	900 912
ClareAJ251507	(705)	ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACCTTG				
huNall18 (AK)	(401)	ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACCTTG				
JeongAF225987	(865)	ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACCTTG				
Consensus	(865)	ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACCTTG				
Section 20						
	(913)	913	920	930	940	950 960
ClareAJ251507	(753)	AGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACCTGGA				
huNall18 (AK)	(449)	AGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACCTGGA				
JeongAF225987	(913)	AGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACCTGGA				
Consensus	(913)	AGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACCTGGA				
Section 21						
	(961)	961	970	980	990	1008
ClareAJ251507	(801)	ATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGC				
huNall18 (AK)	(497)	ATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGC				
JeongAF225987	(961)	ATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGC				
Consensus	(961)	ATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGC				

Section 22

	(1009)	1009	1020	1030	1040	1056
ClareAJ251507	(849)	TTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTC				
huNall18 (AK)	(545)	TTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTC				
JeongAF225987	(1009)	TTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTC				
Consensus	(1009)	TTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTC				

Section 23

	(1057)	1057	1070	1080	1090	1104
ClareAJ251507	(897)	AGTGTCAATTGTGATGGCCTATGTACAGAAATTTGTAGCCCTAGGCAAT				
huNall18 (AK)	(593)	AGTGTCAATTGTGATGGCCTATGTACAGAAATTTGTAGCCCTAGGCAAT				
JeongAF225987	(1057)	AGTGTCAATTGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAAT				
Consensus	(1057)	AGTGTCAATTGTGATGGCGTATGTAACAGAAATTTGTAGCCCTAGGCAAT				

Section 24

	(1105)	1105	1110	1120	1130	1140	1152
ClareAJ251507	(945)	GTCTCAGCGTTTGAACATTCAGAGTCTTGAGAGCTCTGAAAACATT					
huNall18 (AK)	(641)	GTCTCAGCGTTTGAACATTCAGAGTCTTGAGAGCTCTGAAAACATT					
JeongAF225987	(1105)	GTCTCAGCGTTGAGAACATTCAGAGTCTCCGAGCACTGAAAACAATT					
Consensus	(1105)	GTTTCAGCCCTTCGAACATTCAGAGTCTTGAGAGCTCTGAAAACATT					

Section 25

	(1153)	1153	1160	1170	1180	1190	1200
ClareAJ251507	(993)	TCAGTCAATTCAGGTTTAAAGACCATTGTGGGGGCCCTGATCCAGTCG					
huNall18 (AK)	(689)	TCAGTCAATTCAGGTTTAAAGACCATTGTGGGGGCCCTGATCCAGTCG					
JeongAF225987	(1153)	TCAGTCAATTCAGGTTTAAAGACCATTGTGGGGGCCCTGATCCAGTCG					
Consensus	(1153)	TCTGTAATTCAGGTTTAAAGACCATTGTGGGGGCCCTGATCCAGTCG					

Section 26

	(1201)	1201	1210	1220	1230	1248
ClareAJ251507	(1041)	GTAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGC				
huNall18 (AK)	(737)	GTAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGC				
JeongAF225987	(1201)	GTAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGC				
Consensus	(1201)	GTAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGC				

Section 27

	(1249)	1249	1260	1270	1280	1296
ClareAJ251507	(1089)	GTGTTTGCTCTCATTGGGCTGCAGCTGTTTCATGGGCAATCTGAGGAAT				
huNall18 (AK)	(785)	GTGTTTGCTCTCATTGGGCTGCAGCTGTTTCATGGGCAATCTGAGGAAT				
JeongAF225987	(1249)	GTGTTTGCTCTCATTGGGCTGCAGCTGTTTCATGGGCAATCTGAGGAAT				
Consensus	(1249)	GTGTTTGCTCTCATTGGGCTGCAGCTGTTTCATGGGCAATCTGAGGAAT				

Section 28

	(1297)	1297	1310	1320	1330	1344
ClareAJ251507	(1137)	AAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTTTTGAACCAACACC				
huNall18 (AK)	(833)	AAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTTTTGAACCAACACC				
JeongAF225987	(1297)	AAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTTTTGAACCAACACC				
Consensus	(1297)	AAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTTTTGAACCAACACC				

Section 29

	(1345)	1345	1350	1360	1370	1380	1392
ClareAJ251507	(1185)	ACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAAT					
huNall18 (AK)	(881)	ACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAAT					
JeongAF225987	(1345)	ACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAAT					
Consensus	(1345)	ACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAAT					

Section 30

	(1393)	1393	1400	1410	1420	1430	1440
ClareAJ251507	(1233)	GTAACAATGAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGT					
huNall18 (AK)	(929)	GTAACAATGAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGT					
JeongAF225987	(1393)	GTAACAATGAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGT					
Consensus	(1393)	GTAACAATGAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGT					

Section 31

	(1441)	1441	1450	1460	1470	1488
ClareAJ251507	(1281)	CACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAAT				
huNall18 (AK)	(977)	CACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAAT				
JeongAF225987	(1441)	CACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAAT				
Consensus	(1441)	CACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAAT				

Section 32

	(1489)	1489	1500	1510	1520	1536
ClareAJ251507	(1329)	GGCTCAGATGCAGGCCAGTGTCAGAAAGGATACATCTGTGTGAAGGCT				
huNall18 (AK)	(1025)	GGCTCAGATGCAGGCCAGTGTCAGAAAGGATACATCTGTGTGAAGGCT				
JeongAF225987	(1489)	GGCTCAGATGCAGGCCAGTGTCAGAAAGGATACATCTGTGTGAAGGCT				
Consensus	(1489)	GGCTCAGATGCAGGCCAGTGTCAGAAAGGATACATCTGTGTGAAGGCT				

Section 33

	(1537)	1537	1550	1560	1570	1584
ClareAJ251507	(1377)	GGTCGAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGG				
huNall18 (AK)	(1073)	GGTCGAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGG				
JeongAF225987	(1537)	GGTCGAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGG				
Consensus	(1537)	GGTCGAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGG				

Section 34

	(1585)	1585	1590	1600	1610	1620	1632
ClareAJ251507	(1425)	GCTTTCCTGTCTCTATTTTCGACTCATGACTCAAGACTTTGGGAAAAT					
huNall18 (AK)	(1121)	GCTTTCCTGTCTCTATTTTCGACTCATGACTCAAGACTTTGGGAAAAT					
JeongAF225987	(1585)	GCTTTCCTGTCTCTATTTTCGACTCATGACTCAAGACTTTGGGAAAAT					
Consensus	(1585)	GCTTTCCTGTCTCTATTTTCGACTCATGACTCAAGACTTTGGGAAAAT					

Section 35

	(1633)	1633	1640	1650	1660	1670	1680
ClareAJ251507	(1473)	CTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT					
huNall18 (AK)	(1169)	CTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT					
JeongAF225987	(1633)	CTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT					
Consensus	(1633)	CTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT					

						Section 36
(1681)	1681	1690	1700	1710	1728	
ClareAJ251507 (1521)	TTTGTCTCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATC					
huNall18 (AK) (1217)	TTTGTCTCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATC					
JeongAF225987 (1681)	TTTGTCTCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATC					
Consensus (1681)	TTTGTCTCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATC					
						Section 37
(1729)	1729	1740	1750	1760	1776	
ClareAJ251507 (1569)	CTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTG					
huNall18 (AK) (1265)	CTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTG					
JeongAF225987 (1729)	CTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTG					
Consensus (1729)	CTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTG					
						Section 38
(1777)	1777	1790	1800	1810	1824	
ClareAJ251507 (1617)	GAAGAAGCAGAACAAAAAGAGGCCGAATTTTCAGCAGATGCTCGAACAG					
huNall18 (AK) (1313)	GAAGAAGCAGAACAAAAAGAGGCCGAATTTTCAGCAGATGCTCGAACAG					
JeongAF225987 (1777)	GAAGAAGCAGAACAAAAAGAGGCCGAATTTTCAGCAGATGCTCGAACAG					
Consensus (1777)	GAAGAAGCAGAACAAAAAGAGGCCGAATTTTCAGCAGATGCTCGAACAG					
						Section 39
(1825)	1825	1830	1840	1850	1860	1872
ClareAJ251507 (1665)	CTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCT					
huNall18 (AK) (1361)	CTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCT					
JeongAF225987 (1825)	CTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCT					
Consensus (1825)	CTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCT					
						Section 40
(1873)	1873	1880	1890	1900	1910	1920
ClareAJ251507 (1713)	GCTTCAAGAGATTTTCAGTGGAATAGGTGGGTTAGGAGAGCTGTTGGAA					
huNall18 (AK) (1409)	GCTTCAAGAGATTTTCAGTGGAATAGGTGGGTTAGGAGAGCTGTTGGAA					
JeongAF225987 (1873)	GCTTCAAGAGATTTTCAGTGGAATAGGTGGGTTAGGAGAGCTGTTGGAA					
Consensus (1873)	GCTTCAAGAGATTTTCAGTGGAATAGGTGGGTTAGGAGAGCTGTTGGAA					
						Section 41
(1921)	1921	1930	1940	1950	1968	
ClareAJ251507 (1761)	AGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGTGCTAAAGAATGG					
huNall18 (AK) (1457)	AGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGTGCTAAAGAATGG					
JeongAF225987 (1921)	AGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGTGCTAAAGAATGG					
Consensus (1921)	AGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGTGCTAAAGAATGG					
						Section 42
(1969)	1969	1980	1990	2000	2016	
ClareAJ251507 (1809)	AGGAACCGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAAC					
huNall18 (AK) (1505)	AGGAACCGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAAC					
JeongAF225987 (1969)	AGGAACCGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAAC					
Consensus (1969)	AGGAACCGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAAC					

Section 43

	(2017)	2017	2030	2040	2050	2064
ClareAJ251507 (1857)		AACAAAGGAGAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGC				
huNall18 (AK) (1553)		AACAAAGGAGAGAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGC				
JeongAF225987 (2017)		AACAAAGGAGAGAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGC				
Consensus (2017)		AACAAAGGAGAGAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGC				

Section 44

	(2065)	2065	2070	2080	2090	2100	2112
ClareAJ251507 (1905)		GTCAAAGAAGCAGCTTCCTTTTCTCCATGGATGGAAACAGACTGACC					
huNall18 (AK) (1601)		GTCAAAGAAGCAGCTTCCTTTTCTCCATGGATGGAAACAGACTGACC					
JeongAF225987 (2065)		GTCAAAGAAGCAGCTTCCTTTTCTCCATGGATGGAAACAGACTGACC					
Consensus (2065)		GTCAAAGAAGCAGCTTCCTTTTCTCCATGGATGGAAACAGACTGACC					

Section 45

	(2113)	2113	2120	2130	2140	2150	2160
ClareAJ251507 (1953)		AGTGACAAAAAATCTTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGT					
huNall18 (AK) (1649)		AGTGACAAAAAATCTTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGT					
JeongAF225987 (2113)		AGTGACAAAAAATCTTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGT					
Consensus (2113)		AGTGACAAAAAATCTTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGT					

Section 46

	(2161)	2161	2170	2180	2190	2208
ClareAJ251507 (2001)		GGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACAAGCATTTTCAGT				
huNall18 (AK) (1697)		GGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACAAGCATTTTCAGT				
JeongAF225987 (2161)		GGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACAAGCATTTTCAGT				
Consensus (2161)		GGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACAAGCATTTTCAGT				

Section 47

	(2209)	2209	2220	2230	2240	2256
ClareAJ251507 (2049)		TTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGAT				
huNall18 (AK) (1745)		TTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGAT				
JeongAF225987 (2209)		TTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGAT				
Consensus (2209)		TTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGAT				

Section 48

	(2257)	2257	2270	2280	2290	2304
ClareAJ251507 (2097)		GATGAACACAGCACATTTGAAGACGCGAAAGCAGGAGAGACTCACTG				
huNall18 (AK) (1793)		GATGAACACAGCACATTTGAAGACGCGAAAGCAGGAGAGACTCACTG				
JeongAF225987 (2257)		GATGAACACAGCACATTTGAAGACGCGAAAGCAGGAGAGACTCACTG				
Consensus (2257)		GATGAACACAGCACATTTGAAGACAGCGAAAGCAGGAGAGACTCACTG				

Section 49

	(2305)	2305	2310	2320	2330	2340	2352
ClareAJ251507 (2145)		TTTGTGCCGCACAGACATGGAGAGCGACGCAACAGTAACG-----					
huNall18 (AK) (1841)		TTTGTGCCGCACAGACATGGAGAGCGACGCAACAGTAACGTTAGTCAG					
JeongAF225987 (2305)		TTTGTGCCGCACAGACATGGAGAGCGACGCAACAGTAACGTTAGTCAG					
Consensus (2305)		TTTGTGCCGCACAGACATGGAGAGCGACGCAACAGTAACGTTAGTCAG					

Section 50

	(2353)	2353	2360	2370	2380	2390	2400
ClareAJ251507 (2185)		-----					
huNall118 (AK) (1889)		GCCAGTATGTCATCCAGGATGGTGCAGGGCTTCCAGCAAATGGGAAG					
JeongAF225987 (2353)		GCCAGTATGTCATCCAGGATGGTGCAGGGCTTCCAGCAAATGGGAAG					
Consensus (2353)		GCCAGTATGTCATCCAGGATGGTGCAGGGCTTCCAGCAAATGGGAAG					

Section 51

	(2401)	2401	2410	2420	2430	2448
ClareAJ251507 (2185)		-----				
huNall118 (AK) (1937)		ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGTGGA				
JeongAF225987 (2401)		ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGTGGA				
Consensus (2401)		ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGTGGA				

Section 52

	(2449)	2449	2460	2470	2480	2496
ClareAJ251507 (2185)		-----				GCACC
huNall118 (AK) (1985)		CCTTCAGCTCTAACGTCACCTACTGGACAACCTCCCCAGAGGGCACC				GCACC
JeongAF225987 (2449)		CCTTCAGCTCTAACGTCACCTACTGGACAACCTCCCCAGAGGGCACC				GCACC
Consensus (2449)		CCTTCAGCTCTAACGTCACCTACTGGACAACCTCCCCAGAGGGCACC				GCACC

Section 53

	(2497)	2497	2510	2520	2530	2544
ClareAJ251507 (2190)		ACCACGAAACGGAAGTCAGAAAGAGAAGGTTAAGCTCTTACCAGATT				
huNall118 (AK) (2033)		ACCACAGAAACGGAAGTCAGAAAGAGAAGGTTAAGCTCTTACCAGATT				
JeongAF225987 (2497)		ACCACGAAACGGAAGTCAGAAAGAGAAGGTTAAGCTCTTACCAGATT				
Consensus (2497)		ACCACTGAAACGGAAGTCAGAAAGAGAAGGTTAAGCTCTTACCAGATT				

Section 54

	(2545)	2545	2550	2560	2570	2580	2592
ClareAJ251507 (2238)		TCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCCAAGAGCCGTGAGC					
huNall118 (AK) (2081)		TCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCCAAGAGCCGTGAGC					
JeongAF225987 (2545)		TCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCCAAGAGCCGTGAGC					
Consensus (2545)		TCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCCAAGAGCCGTGAGC					

Section 55

	(2593)	2593	2600	2610	2620	2630	2640
ClareAJ251507 (2286)		ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGA					
huNall118 (AK) (2129)		ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGA					
JeongAF225987 (2593)		ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGA					
Consensus (2593)		ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGA					

Section 56

	(2641)	2641	2650	2660	2670	2688
ClareAJ251507 (2334)		CAGAAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATC				
huNall118 (AK) (2177)		CAGAAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATC				
JeongAF225987 (2641)		CAGAAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATC				
Consensus (2641)		CAGAAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATC				

Section 57

	(2689)	2689	2700	2710	2720	2736
ClareAJ251507 (2382)		TGGGACTGCTGTGATGCATGGTTAAAAGTAAACATCTTGTGAATTTA				
huNall18 (AK) (2225)		TGGGACTGCTGTGATGCATGGTTAAAAGTAAACATCTTGTGAATTTA				
JeongAF225987 (2689)		TGGGACTGCTGTGATGCATGGTTAAAAGTAAACATCTTGTGAATTTA				
Consensus (2689)		TGGGACTGCTGTGATGCATGGTTAAAAGTAAACATCTTGTGAATTTA				

Section 58

	(2737)	2737	2750	2760	2770	2784
ClareAJ251507 (2430)		ATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTC				
huNall18 (AK) (2273)		ATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTC				
JeongAF225987 (2737)		ATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTC				
Consensus (2737)		ATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTC				

Section 59

	(2785)	2785	2790	2800	2810	2820	2832
ClareAJ251507 (2478)		TTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA					
huNall18 (AK) (2321)		TTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA					
JeongAF225987 (2785)		TTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA					
Consensus (2785)		TTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA					

Section 60

	(2833)	2833	2840	2850	2860	2870	2880
ClareAJ251507 (2526)		TTCAGTAGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTC					
huNall18 (AK) (2369)		TTCAGTAGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTC					
JeongAF225987 (2833)		TTCAGTAGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTC					
Consensus (2833)		TTCAGTAGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTC					

Section 61

	(2881)	2881	2890	2900	2910	2928
ClareAJ251507 (2574)		ACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTAT				
huNall18 (AK) (2417)		ACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTAT				
JeongAF225987 (2881)		ACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTAT				
Consensus (2881)		ACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTAT				

Section 62

	(2929)	2929	2940	2950	2960	2976
ClareAJ251507 (2622)		TTCCAAGAAGGCTGGAATATCTTTGATGGAATTATTGTCAGCCTCAGT				
huNall18 (AK) (2465)		TTCCAAGAAGGCTGGAATATCTTTGATGGAATTATTGTCAGCCTCAGT				
JeongAF225987 (2929)		TTCCAAGAAGGCTGGAATATCTTTGATGGAATTATTGTCAGCCTCAGT				
Consensus (2929)		TTCCAAGAAGGCTGGAATATCTTTGATGGAATTATTGTCAGCCTCAGT				

Section 63

	(2977)	2977	2990	3000	3010	3024
ClareAJ251507 (2670)		TTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTGTCTGTACTGCGA				
huNall18 (AK) (2513)		TTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTGTCTGTACTGCGA				
JeongAF225987 (2977)		TTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTGTCTGTACTGCGA				
Consensus (2977)		TTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTGTCTGTACTGCGA				

Section 64

	(3025)	3025	3030	3040	3050	3060	3072
ClareAJ251507 (2718)		TCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA					
huNall18 (AK) (2561)		TCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA					
JeongAF225987 (3025)		TCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA					
Consensus (3025)		TCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA					

Section 65

	(3073)	3073	3080	3090	3100	3110	3120
ClareAJ251507 (2766)		CTAAATATGCTAATTAAGATCATTTGGCAATTCTGTGGGGGCTCTAGGA					
huNall18 (AK) (2609)		CTAAATATGCTAATTAAGATCATTTGGCAATTCTGTGGGGGCTCTAGGA					
JeongAF225987 (3073)		CTAAATATGCTAATTAAGATCATTTGGCAATTCTGTGGGGGCTCTAGGA					
Consensus (3073)		CTAAATATGCTAATTAAGATCATTTGGCAATTCTGTGGGGGCTCTAGGA					

Section 66

	(3121)	3121	3130	3140	3150	3168
ClareAJ251507 (2814)		AACCTCACCTTGGTGTGGCCATCATCGTCTTCATTTTTGCTGTGGTC				
huNall18 (AK) (2657)		AACCTCACCTTGGTGTGGCCATCATCGTCTTCATTTTTGCTGTGGTC				
JeongAF225987 (3121)		AACCTCACCTTGGTGTGGCCATCATCGTCTTCATTTTTGCTGTGGTC				
Consensus (3121)		AACCTCACCTTGGTGTGGCCATCATCGTCTTCATTTTTGCTGTGGTC				

Section 67

	(3169)	3169	3180	3190	3200	3216
ClareAJ251507 (2862)		GGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATC				
huNall18 (AK) (2705)		GGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATC				
JeongAF225987 (3169)		GGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATC				
Consensus (3169)		GGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATC				

Section 68

	(3217)	3217	3230	3240	3250	3264
ClareAJ251507 (2910)		AATGATGACTGTACGCTCCACGGTGGCACATGAACGACTTCTTCCAC				
huNall18 (AK) (2753)		AATGATGACTGTACGCTCCACGGTGGCACATGAACGACTTCTTCCAC				
JeongAF225987 (3217)		AATGATGACTGTACGCTCCACGGTGGCACATGAACGACTTCTTCCAC				
Consensus (3217)		AATGATGACTGTACGCTCCACGGTGGCACATGAACGACTTCTTCCAC				

Section 69

	(3265)	3265	3270	3280	3290	3300	3312
ClareAJ251507 (2958)		TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC					
huNall18 (AK) (2801)		TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC					
JeongAF225987 (3265)		TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC					
Consensus (3265)		TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC					

Section 70

	(3313)	3313	3320	3330	3340	3350	3360
ClareAJ251507 (3006)		ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTT					
huNall18 (AK) (2849)		ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTT					
JeongAF225987 (3313)		ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTT					
Consensus (3313)		ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTT					

Section 71					
	(3361)	3361	3370	3380	3390 3408
ClareAJ251507 (3054)		TTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTT			
huNall18 (AK) (2897)		TTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTT			
JeongAF225987 (3361)		TTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTT			
Consensus (3361)		TTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTT			
Section 72					
	(3409)	3409	3420	3430	3440 3456
ClareAJ251507 (3102)		CTGGCCTTATTGTTGAGTTCATTTAGCTCAGACAACCTTGCTGCTACT			
huNall18 (AK) (2945)		CTGGCCTTATTGTTGAGTTCATTTAGCTCAGACAACCTTGCTGCTACT			
JeongAF225987 (3409)		CTGGCCTTATTGTTGAGTTCATTTAGCTCAGACAACCTTGCTGCTACT			
Consensus (3409)		CTGGCCTTATTGTTGAGTTCATTTAGCTCAGACAACCTTGCTGCTACT			
Section 73					
	(3457)	3457	3470	3480	3490 3504
ClareAJ251507 (3150)		GATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATG			
huNall18 (AK) (2993)		GATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATG			
JeongAF225987 (3457)		GATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATG			
Consensus (3457)		GATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATG			
Section 74					
	(3505)	3505	3510	3520	3530 3540 3552
ClareAJ251507 (3198)		CAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA			
huNall18 (AK) (3041)		CAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA			
JeongAF225987 (3505)		CAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA			
Consensus (3505)		CAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA			
Section 75					
	(3553)	3553	3560	3570	3580 3590 3600
ClareAJ251507 (3246)		AAAGCCTTTTTTAGAAAGCCAAAAGTTATAGAAATCCATGAAGGCAAT			
huNall18 (AK) (3089)		AAAGCCTTTTTTAGAAAGCCAAAAGTTATAGAAATCCATGAAGGCAAT			
JeongAF225987 (3553)		AAAGCCTTTTTTAGAAAGCCAAAAGTTATAGAAATCCATGAAGGCAAT			
Consensus (3553)		AAAGCCTTTTTTAGAAAGCCAAAAGTTATAGAAATCCATGAAGGCAAT			
Section 76					
	(3601)	3601	3610	3620	3630 3648
ClareAJ251507 (3294)		AAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAA			
huNall18 (AK) (3137)		AAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAA			
JeongAF225987 (3601)		AAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAA			
Consensus (3601)		AAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAA			
Section 77					
	(3649)	3649	3660	3670	3680 3696
ClareAJ251507 (3342)		GAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGT			
huNall18 (AK) (3185)		GAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGT			
JeongAF225987 (3649)		GAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGT			
Consensus (3649)		GAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGT			

Section 78

	(3697)	3697	3710	3720	3730	3744
ClareAJ251507 (3390)		ACTGGAAGCAGT	GTTGAAAAATACGTAATCGATGAAAATGATTATATG			
huNall18 (AK) (3233)		ACTGGAAGCAGT	GTTGAAAAATACGTAATCGATGAAAATGATTATATG			
JeongAF225987 (3697)		ACTGGAAGCAGT	GTTGAAAAATACGTAATCGATGAAAATGATTATATG			
Consensus (3697)		ACTGGAAGCAGT	GTTGAAAAATACGTAATCGATGAAAATGATTATATG			

Section 79

	(3745)	3745	3750	3760	3770	3780	3792
ClareAJ251507 (3438)		TCATTCATAAACAACCCCAGCCTCACCGTCACAGTGCCAATTGCTGTT					
huNall18 (AK) (3281)		TCATTCATAAACAACCCCAGCCTCACCGTCACAGTGCCAATTGCTGTT					
JeongAF225987 (3745)		TCATTCATAAACAACCCCAGCCTCACCGTCACAGTGCCAATTGCTGTT					
Consensus (3745)		TCATTCATAAACAACCCCAGCCTCACCGTCACAGTGCCAATTGCTGTT					

Section 80

	(3793)	3793	3800	3810	3820	3830	3840
ClareAJ251507 (3486)		GGAGAGTCTGACTTTGAAAACCTAAATACTGAAGAGTTCAGCAGTGAG					
huNall18 (AK) (3329)		GGAGAGTCTGACTTTGAAAACCTAAATACTGAAGAGTTCAGCAGTGAG					
JeongAF225987 (3793)		GGAGAGTCTGACTTTGAAAACCTAAATACTGAAGAGTTCAGCAGTGAG					
Consensus (3793)		GGAGAGTCTGACTTTGAAAACCTAAATACTGAAGAGTTCAGCAGTGAG					

Section 81

	(3841)	3841	3850	3860	3870	3888
ClareAJ251507 (3534)		TCAGAAGTAGAAGAAAGCAAAGAGAAATTAAATGCAACCAGCTCATCT				
huNall18 (AK) (3377)		TCAGAAGTAGAAGAAAGCAAAGAGAAATTAAATGCAACCAGCTCATCT				
JeongAF225987 (3841)		TCAGAAGTAGAAGAAAGCAAAGAGAAATTAAATGCAACCAGCTCATCT				
Consensus (3841)		TCAGAAGTAGAAGAAAGCAAAGAGAAATTAAATGCAACCAGCTCATCT				

Section 82

	(3889)	3889	3900	3910	3920	3936
ClareAJ251507 (3582)		GAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCT				
huNall18 (AK) (3425)		GAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCT				
JeongAF225987 (3889)		GAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCT				
Consensus (3889)		GAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCT				

Section 83

	(3937)	3937	3950	3960	3970	3984
ClareAJ251507 (3630)		GAAACTGAACCCGAAGAAGACCTTAAACCGGAAGCTTGTTTTACTGAA				
huNall18 (AK) (3473)		GAAACTGAACCCGAAGAAGACCTTAAACCGGAAGCTTGTTTTACTGAA				
JeongAF225987 (3937)		GAAACTGAACCCGAAGAAGACCTTAAACCGGAAGCTTGTTTTACTGAA				
Consensus (3937)		GAAACTGAACCCGAAGAAGACCTTAAACCGGAAGCTTGTTTTACTGAA				

Section 84

	(3985)	3985	3990	4000	4010	4020	4032
ClareAJ251507 (3678)		GGTGTATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGC					
huNall18 (AK) (3521)		GGTGTATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGC					
JeongAF225987 (3985)		GGTGTATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGC					
Consensus (3985)		GGTGTATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGC					

Section 85

	(4033)	4033	4040	4050	4060	4070	4080
ClareAJ251507 (3726)		AAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGTATTGTT					
huNall18 (AK) (3569)		AAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGTATTGTT					
JeongAF225987 (4033)		AAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGTATTGTT					
Consensus (4033)		AAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGTATTGTT					

Section 86

	(4081)	4081	4090	4100	4110	4128
ClareAJ251507 (3774)		GAGCACAACTGGTTTGAGACTTTTCATTGTGTTTCATGATCCTTCTCAGT				
huNall18 (AK) (3617)		GAGCACAACTGGTTTGAGACTTTTCATTGTGTTTCATGATCCTTCTCAGT				
JeongAF225987 (4081)		GAGCACAACTGGTTTGAGACTTTTCATTGTGTTTCATGATCCTTCTCAGT				
Consensus (4081)		GAGCACAACTGGTTTGAGACTTTTCATTGTGTTTCATGATCCTTCTCAGT				

Section 87

	(4129)	4129	4140	4150	4160	4176
ClareAJ251507 (3822)		AGTGGTGCATTGGCCCTTTGAAGATATATACATTGAACAGCGAAAGACT				
huNall18 (AK) (3665)		AGTGGTGCATTGGCCCTTTGAAGATATATACATTGAACAGCGAAAGACT				
JeongAF225987 (4129)		AGTGGTGCATTGGCCCTTTGAAGATATATACATTGAACAGCGAAAGACT				
Consensus (4129)		AGTGGTGCATTGGCCCTTTGAAGATATATACATTGAACAGCGAAAGACT				

Section 88

	(4177)	4177	4190	4200	4210	4224
ClareAJ251507 (3870)		ATCAAAACCATGCTAGAAATATGCTGACAAAGTCTTTACCTATATATATTC				
huNall18 (AK) (3713)		ATCAAAACCATGCTAGAAATATGCTGACAAAGTCTTTACCTATATATATTC				
JeongAF225987 (4177)		ATCAAAACCATGCTAGAAATATGCTGACAAAGTCTTTACCTATATATATTC				
Consensus (4177)		ATCAAAACCATGCTAGAAATATGCTGACAAAGTCTTTACCTATATATATTC				

Section 89

	(4225)	4225	4230	4240	4250	4260	4272
ClareAJ251507 (3918)		ATTCTGGAAATGCTTCTCAAATGGGTGCTTATGGATTTCAAACATAT					
huNall18 (AK) (3761)		ATTCTGGAAATGCTTCTCAAATGGGTGCTTATGGATTTCAAACATAT					
JeongAF225987 (4225)		ATTCTGGAAATGCTTCTCAAATGGGTGCTTATGGATTTCAAACATAT					
Consensus (4225)		ATTCTGGAAATGCTTCTCAAATGGGTGCTTATGGATTTCAAACATAT					

Section 90

	(4273)	4273	4280	4290	4300	4310	4320
ClareAJ251507 (3966)		TTCACCTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCT					
huNall18 (AK) (3809)		TTCACCTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCT					
JeongAF225987 (4273)		TTCACCTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCT					
Consensus (4273)		TTCACCTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCT					

Section 91

	(4321)	4321	4330	4340	4350	4368
ClareAJ251507 (4014)		TTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCC				
huNall18 (AK) (3857)		TTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCC				
JeongAF225987 (4321)		TTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCC				
Consensus (4321)		TTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCC				

Section 92

	(4369)	4369	4380	4390	4400	4416
ClareAJ251507	(4062)	ATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTA				
huNall18 (AK)	(3905)	ATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTA				
JeongAF225987	(4369)	ATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTA				
Consensus	(4369)	ATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTA				

Section 93

	(4417)	4417	4430	4440	4450	4464
ClareAJ251507	(4110)	TCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCA				
huNall18 (AK)	(3953)	TCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCA				
JeongAF225987	(4417)	TCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCA				
Consensus	(4417)	TCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCA				

Section 94

	(4465)	4465	4470	4480	4490	4500	4512
ClareAJ251507	(4158)	ATTCCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTG					
huNall18 (AK)	(4001)	ATTCCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTG					
JeongAF225987	(4465)	ATTCCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTG					
Consensus	(4465)	ATTCCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTG					

Section 95

	(4513)	4513	4520	4530	4540	4550	4560
ClareAJ251507	(4206)	ATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTCTACCAC					
huNall18 (AK)	(4049)	ATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTCTACCAC					
JeongAF225987	(4513)	ATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTCTACCAC					
Consensus	(4513)	ATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTCTACCAC					

Section 96

	(4561)	4561	4570	4580	4590	4608
ClareAJ251507	(4254)	TGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAAC				
huNall18 (AK)	(4097)	TGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAAC				
JeongAF225987	(4561)	TGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAAC				
Consensus	(4561)	TGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAAC				

Section 97

	(4609)	4609	4620	4630	4640	4656
ClareAJ251507	(4302)	AATTTGAGTGACTGTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAAC				
huNall18 (AK)	(4145)	AATTTGAGTGACTGTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAAC				
JeongAF225987	(4609)	AATTTGAGTGACTGTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAAC				
Consensus	(4609)	AATTTGAGTGACTGTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAAC				

Section 98

	(4657)	4657	4670	4680	4690	4704
ClareAJ251507	(4350)	GTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTT				
huNall18 (AK)	(4193)	GTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTT				
JeongAF225987	(4657)	GTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTT				
Consensus	(4657)	GTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTT				

Section 99

	(4705)	4705	4710	4720	4730	4740	4752
ClareAJ251507 (4398)		CAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTT					
huNaIII18 (AK) (4241)		CAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTT					
JeongAF225987 (4705)		CAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTT					
Consensus (4705)		CAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTT					

Section 100

	(4753)	4753	4760	4770	4780	4790	4800
ClareAJ251507 (4446)		GATTCACGAGATGTTAAACTTCAGCCTGTATATGAAGAAAATCTGTAC					
huNaIII18 (AK) (4289)		GATTCACGAGATGTTAAACTTCAGCCTGTATATGAAGAAAATCTGTAC					
JeongAF225987 (4753)		GATTCACGAGATGTTAAACTTCAGCCTGTATATGAAGAAAATCTGTAC					
Consensus (4753)		GATTCACGAGATGTTAAACTTCAGCCTGTATATGAAGAAAATCTGTAC					

Section 101

	(4801)	4801	4810	4820	4830	4848
ClareAJ251507 (4494)		ATGTATTTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTCACT				
huNaIII18 (AK) (4337)		ATGTATTTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTCACT				
JeongAF225987 (4801)		ATGTATTTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTCACT				
Consensus (4801)		ATGTATTTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTCACT				

Section 102

	(4849)	4849	4860	4870	4880	4896
ClareAJ251507 (4542)		CTGAATCTATTTCATTGGTGTTCATCATAGATAACTTCAACCAGCAGAAA				
huNaIII18 (AK) (4385)		CTGAATCTATTTCATTGGTGTTCATCATAGATAACTTCAACCAGCAGAAA				
JeongAF225987 (4849)		CTGAATCTATTTCATTGGTGTTCATCATAGATAACTTCAACCAGCAGAAA				
Consensus (4849)		CTGAATCTATTTCATTGGTGTTCATCATAGATAACTTCAACCAGCAGAAA				

Section 103

	(4897)	4897	4910	4920	4930	4944
ClareAJ251507 (4590)		AAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAA				
huNaIII18 (AK) (4433)		AAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAA				
JeongAF225987 (4897)		AAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAA				
Consensus (4897)		AAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAA				

Section 104

	(4945)	4945	4950	4960	4970	4980	4992
ClareAJ251507 (4638)		TATTACAATGCAATGAAGAACTTGGATCCAAGAAACCTCAGAAACCC					
huNaIII18 (AK) (4481)		TATTACAATGCAATGAAGAACTTGGATCCAAGAAACCTCAGAAACCC					
JeongAF225987 (4945)		TATTACAATGCAATGAAGAACTTGGATCCAAGAAACCTCAGAAACCC					
Consensus (4945)		TATTACAATGCAATGAAGAACTTGGATCCAAGAAACCTCAGAAACCC					

Section 105

	(4993)	4993	5000	5010	5020	5030	5040
ClareAJ251507 (4686)		ATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTA					
huNaIII18 (AK) (4529)		ATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTA					
JeongAF225987 (4993)		ATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTA					
Consensus (4993)		ATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTA					

Section 106

	(5041)	5041	5050	5060	5070	5088
ClareAJ251507 (4734)		ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAAC				
huNall18 (AK) (4577)		ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAAC				
JeongAF225987 (5041)		ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAAC				
Consensus (5041)		ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAAC				

Section 107

	(5089)	5089	5100	5110	5120	5136
ClareAJ251507 (4782)		ATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACC				
huNall18 (AK) (4625)		ATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACC				
JeongAF225987 (5089)		ATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACC				
Consensus (5089)		ATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACC				

Section 108

	(5137)	5137	5150	5160	5170	5184
ClareAJ251507 (4830)		CTAGTTTGTGCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGA				
huNall18 (AK) (4673)		CTAGTTTGTGCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGA				
JeongAF225987 (5137)		CTAGTTTGTGCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGA				
Consensus (5137)		CTAGTTTGTGCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGA				

Section 109

	(5185)	5185	5190	5200	5210	5220	5232
ClareAJ251507 (4878)		GAATTTGTGCTGAAGCTCGTTCCCTCAGACACTACTACTTCACTATA					
huNall18 (AK) (4721)		GAATTTGTGCTGAGGCTCGTTCCCTCAGACACTACTACTTCACTATA					
JeongAF225987 (5185)		GAATTTGTGCTGAAGCTCGTTCCCTCAGACACTACTACTTCACTATA					
Consensus (5185)		GAATTTGTGCTGAAGCTCGTCTCCCTCAGACACTACTACTTCACTATA					

Section 110

	(5233)	5233	5240	5250	5260	5270	5280
ClareAJ251507 (4926)		GGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGT					
huNall18 (AK) (4769)		GGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGT					
JeongAF225987 (5233)		GGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGT					
Consensus (5233)		GGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGT					

Section 111

	(5281)	5281	5290	5300	5310	5328
ClareAJ251507 (4974)		ATGTTTCTGGCTGAGATGATAGAAAAGTATTCTGTGTCCCCTACCTTG				
huNall18 (AK) (4817)		ATGTTTCTGGCTGAGATGATAGAAAAGTATTCTGTGTCCCCTACCTTG				
JeongAF225987 (5281)		ATGTTTCTGGCTGAGATGATAGAAAAGTATTCTGTGTCCCCTACCTTG				
Consensus (5281)		ATGTTTCTGGCTGAGATGATAGAAAAGTATTTTGTGTCCCCTACCTTG				

Section 112

	(5329)	5329	5340	5350	5360	5376
ClareAJ251507 (5022)		TTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATC				
huNall18 (AK) (4865)		TTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATC				
JeongAF225987 (5329)		TTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATC				
Consensus (5329)		TTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATC				

Section 113						
	(5377)	5377	5390	5400	5410	5424
ClareAJ251507 (5070)		AAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCC				
huNall18 (AK) (4913)		AAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCC				
JeongAF225987 (5377)		AAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCC				
Consensus (5377)		AAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCC				
Section 114						
	(5425)	5425	5430	5440	5450	5472
ClareAJ251507 (5118)		CTTCCTGCGTTGTTTAAACATCGGCCTCCTGCTCTTCCTGGTCATGTTT				
huNall18 (AK) (4961)		CTTCCTGCGTTGTTTAAACATCGGCCTCCTGCTCTTCCTGGTCATGTTT				
JeongAF225987 (5425)		CTTCCTGCGTTGTTTAAACATCGGCCTCCTGCTCTTCCTGGTCATGTTT				
Consensus (5425)		CTTCCTGCGTTGTTTAAACATCGGCCTCCTGCTCTTCCTGGTCATGTTT				
Section 115						
	(5473)	5473	5480	5490	5500	5520
ClareAJ251507 (5166)		ATCTATGCCATCTTTGGGATGTCCAACCTTGCCTATGTTAAAAAGGAA				
huNall18 (AK) (5009)		ATCTATGCCATCTTTGGGATGTCCAACCTTGCCTATGTTAAAAAGGAA				
JeongAF225987 (5473)		ATCTATGCCATCTTTGGGATGTCCAACCTTGCCTATGTTAAAAAGGAA				
Consensus (5473)		ATCTATGCCATCTTTGGGATGTCCAACCTTGCCTATGTTAAAAAGGAA				
Section 116						
	(5521)	5521	5530	5540	5550	5568
ClareAJ251507 (5214)		GCTGGAATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATG				
huNall18 (AK) (5057)		GCTGGAATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATG				
JeongAF225987 (5521)		GCTGGAATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATG				
Consensus (5521)		GCTGGAATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATG				
Section 117						
	(5569)	5569	5580	5590	5600	5616
ClareAJ251507 (5262)		ATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTA				
huNall18 (AK) (5105)		ATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTA				
JeongAF225987 (5569)		ATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTA				
Consensus (5569)		ATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTA				
Section 118						
	(5617)	5617	5630	5640	5650	5664
ClareAJ251507 (5310)		GCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATT				
huNall18 (AK) (5153)		GCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATT				
JeongAF225987 (5617)		GCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATT				
Consensus (5617)		GCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATT				
Section 119						
	(5665)	5665	5670	5680	5690	5712
ClareAJ251507 (5358)		CACCCTGGCAGCTCAGTTAAGGGAGACGTTGGGACCCATCTGTTGGG				
huNall18 (AK) (5201)		CACCCTGGCAGCTCAGTTAAGGGAGACGTTGGGACCCATCTGTTGGG				
JeongAF225987 (5665)		CACCCTGGCAGCTCAGTTAAGGGAGACCGTGGGGACCCATCTGTTGGG				
Consensus (5665)		CACCCTGGCAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGG				

Section 120

	(5713)	5713	5720	5730	5740	5750	5760
ClareAJ251507 (5406)		ATTTTCTTTTTT	CGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTG				
huNall18 (AK) (5249)		ATTTTCTTTTTT	CGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTG				
JeongAF225987 (5713)		ATTTTCTTTTTT	CGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTG				
Consensus (5713)		ATTTTCTTTTTT	TGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTG				

Section 121

	(5761)	5761	5770	5780	5790	5808
ClareAJ251507 (5454)		AACATGTACATCGCGGTCATCCTGGGAGAACTTCAGTGTTGCTACTGAA				
huNall18 (AK) (5297)		AACATGTACATCGCGGTCATCCTGGGAGAACTTCAGTGTTGCTACTGAA				
JeongAF225987 (5761)		AACATGTACATCGCGGTCATCCTGGGAGAACTTCAGTGTTGCTACTGAA				
Consensus (5761)		AACATGTACATCGCGGTCATCCTGGGAGAACTTCAGTGTTGCTACTGAA				

Section 122

	(5809)	5809	5820	5830	5840	5856
ClareAJ251507 (5502)		GAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAG				
huNall18 (AK) (5345)		GAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAG				
JeongAF225987 (5809)		GAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAG				
Consensus (5809)		GAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAG				

Section 123

	(5857)	5857	5870	5880	5890	5904
ClareAJ251507 (5550)		GTTTGGGAAAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCT				
huNall18 (AK) (5393)		GTTTGGGAAAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCT				
JeongAF225987 (5857)		GTTTGGGAAAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCT				
Consensus (5857)		GTTTGGGAAAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCT				

Section 124

	(5905)	5905	5910	5920	5930	5940	5952
ClareAJ251507 (5598)		AAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAGCA					
huNall18 (AK) (5441)		AAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAGCA					
JeongAF225987 (5905)		AAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAGCA					
Consensus (5905)		AAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAGCA					

Section 125

	(5953)	5953	5960	5970	5980	5990	6000
ClareAJ251507 (5646)		AAACCCAACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGT					
huNall18 (AK) (5489)		AAACCCAACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGT					
JeongAF225987 (5953)		AAACCCAACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGT					
Consensus (5953)		AAACCCAACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGT					

Section 126

	(6001)	6001	6010	6020	6030	6048
ClareAJ251507 (5694)		GGTGACCGGATCCACTGTCCTTGATATTTTATTTGCCTTTACAAAGCGT				
huNall18 (AK) (5537)		GGTGACCGGATCCACTGTCCTTGATATTTTATTTGCCTTTACAAAGCGT				
JeongAF225987 (6001)		GGTGACCGGATCCACTGTCCTTGATATTTTATTTGCCTTTACAAAGCGT				
Consensus (6001)		GGTGACCGGATCCACTGTCCTTGATATTTTATTTGCCTTTACAAAGCGT				

Section 127

	(6049)	6049	6060	6070	6080	6096
ClareAJ251507 (5742)		GTTTTG	GTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAA			
huNall18 (AK) (5585)		GTTTTG	GTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAA			
JeongAF225987 (6049)		GTTTTG	GTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAA			
Consensus (6049)		GTTTTG	GGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAA			

Section 128

	(6097)	6097	6110	6120	6130	6144
ClareAJ251507 (5790)		GACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATT				
huNall18 (AK) (5633)		GACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATT				
JeongAF225987 (6097)		GACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATT				
Consensus (6097)		GACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATT				

Section 129

	(6145)	6145	6150	6160	6170	6180	6192
ClareAJ251507 (5838)		ACAACCACTTTGAAACGTAAACAAGAGGAGGTGTCTGCCGCTATCATT					
huNall18 (AK) (5681)		ACAACCACTTTGAAACGTAAACAAGAGGAGGTGTCTGCCGCTATCATT					
JeongAF225987 (6145)		ACAACCACTTTGAAACGTAAACAAGAGGAGGTGTCTGCCGCTATCATT					
Consensus (6145)		ACAACCACTTTGAAACGTAAACAAGAGGAGGTGTCTGCCGCTATCATT					

Section 130

	(6193)	6193	6200	6210	6220	6230	6240
ClareAJ251507 (5886)		CAGCGTAATTTTCAGATGTTATCTTTTAAAGCAAAGGTTAAAAAATATA					
huNall18 (AK) (5729)		CAGCGTAATTTTCAGATGTTATCTTTTAAAGCAAAGGTTAAAAAATATA					
JeongAF225987 (6193)		CAGCGTAATTTTCAGATGTTATCTTTTAAAGCAAAGGTTAAAAAATATA					
Consensus (6193)		CAGCGTAATTTTCAGATGTTATCTTTTAAAGCAAAGGTTAAAAAATATA					

Section 131

	(6241)	6241	6250	6260	6270	6288
ClareAJ251507 (5934)		TCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCT				
huNall18 (AK) (5777)		TCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCT				
JeongAF225987 (6241)		TCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCT				
Consensus (6241)		TCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCT				

Section 132

	(6289)	6289	6300	6310	6320	6336
ClareAJ251507 (5982)		ATAAAAACAAGACATGATTATTGACAAACTAAATGGGAACCTCCACTCCA				
huNall18 (AK) (5825)		ATAAAAACAAGACATGATTATTGACAAACTAAATGGGAACCTCCACTCCA				
JeongAF225987 (6289)		ATAAAAACAAGACATGATTATTGACAAACTAAATGGGAACCTCCACTCCA				
Consensus (6289)		ATAAAAACAAGACATGATTATTGACAAACTAAATGGGAACCTCCACTCCA				

Section 133

	(6337)	6337	6350	6360	6370	6384
ClareAJ251507 (6030)		GAAAAAACAGATGGGAGTTCCTCTACCACC				CTCCTCCTTCCTATGAT
huNall18 (AK) (5873)		GAAAAAACAGATGGGAGTTCCTCTACCACC				CTCCTCCTTCCTATGAT
JeongAF225987 (6337)		GAAAAAACAGATGGGAGTTCCTCTACCACCCTCCTCCTTCCTATGAT				
Consensus (6337)		GAAAAAACAGATGGGAGTTCCTCTACCACCTCCTCCTTCCTATGAT				

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Section 141					
	(6721)	6721	6730	6740	6750 6768
ClareAJ251507 (6414)		GGCTACCTAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAAC			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6721)		GGCTACCTAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAAC			
Consensus (6721)		GGCTACCTAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAAC			
Section 142					
	(6769)	6769	6780	6790	6800 6816
ClareAJ251507 (6462)		CACCAAACACCTTTAGTACAGTCCTTGCATCCATTCTATTTTAACTT			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6769)		CACCAAACACCTTTAGTACAGTCCTTGCATCCATTCTATTTTAACTT			
Consensus (6769)		CACCAAACACCTTTAGTACAGTCCTTGCATCCATTCTATTTTAACTT			
Section 143					
	(6817)	6817	6830	6840	6850 6864
ClareAJ251507 (6510)		CCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCATTTCCATGG			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6817)		CCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCATTTCCATGG			
Consensus (6817)		CCATATCTGCCATATTTTACAAAATTTGTTCTAGTGCATTTCCATGG			
Section 144					
	(6865)	6865	6870	6880	6890 6900 6912
ClareAJ251507 (6558)		TCCCAATTTCATAGTTTATTCATAATGCTATGTCACATTTT			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6865)		TCCCAATTTCATAGTTTATTCATAATGCTATGTCACATTTT			
Consensus (6865)		TCCCAATTTCATAGTTTATTCATAATGCTATGTCACATTTT			
Section 145					
	(6913)	6913	6920	6930	6940 6950 6960
ClareAJ251507 (6600)		-----			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6913)		TGAGGTTTACGTTGAAGAAACAGTATACAAGAACCCTGTCTCTCAAAT			
Consensus (6913)		TGAGGTTTACGTTGAAGAAACAGTATACAAGAACCCTGTCTCTCAAAT			
Section 146					
	(6961)	6961	6970	6980	6990 7008
ClareAJ251507 (6600)		-----			
huNall18 (AK) (6090)		-----			
JeongAF225987 (6961)		GATCAGACAAAGGTGTTTTGCCAGAGAGATAAAATTTTGTCTCAAAC			
Consensus (6961)		GATCAGACAAAGGTGTTTTGCCAGAGAGATAAAATTTTGTCTCAAAC			
Section 147					
	(7009)	7009	7020	7030	7040 7056
ClareAJ251507 (6600)		-----			
huNall18 (AK) (6090)		-----			
JeongAF225987 (7009)		CAGAAAAAGAATTGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTA			
Consensus (7009)		CAGAAAAAGAATTGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTA			

						Section 148
(7057)	7057	7070	7080	7090	7104	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7057)	GATGGCTTTAATTTTGAAAGTATTTTAGTCTGTTATGTTTGTTTCTAT					
Consensus (7057)						
						Section 149
(7105)	7105	7110	7120	7130	7140	7152
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7105)	CTGAACAGTTATGTGCCTGTAAAGTCTCCTCTAATATTTAAAGGATTA					
Consensus (7105)						
						Section 150
(7153)	7153	7160	7170	7180	7190	7200
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7153)	TTTTTATGCAAAGTATTCTGTTTCAGCAAGTGCAAATTTTATTCTAAG					
Consensus (7153)						
						Section 151
(7201)	7201	7210	7220	7230	7248	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7201)	TTTCAGAGCTCTATATTTAATTTAGGTCAAATGCTTTCCAAAAGTAA					
Consensus (7201)						
						Section 152
(7249)	7249	7260	7270	7280	7296	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7249)	TCTAATAAATCCATTCTAGAAAAATATATCTAAAGTATTGCTTTAGAA					
Consensus (7249)						
						Section 153
(7297)	7297	7310	7320	7330	7344	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7297)	TAGTTGTTCCACTTTCTGCTGCAGTATTGCTTTGCCATCTTCTGCTCT					
Consensus (7297)						
						Section 154
(7345)	7345	7350	7360	7370	7380	7392
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7345)	CAGCAAAGCTGATAGTCTATGTCAATTAAATACCTATGTTATGTAAA					
Consensus (7345)						

Section 155						
(7393)	7393	7400	7410	7420	7430	7440
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7393)	TAGTTATTTTATCCTGTGGTGCATGTTTGGGCAAATATATATATAGCC					
Consensus (7393)						
Section 156						
(7441)	7441	7450	7460	7470		7488
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7441)	TGATAAACAACTTCTATTAAATCAAATATGTACCACAGTGTATGTGTC					
Consensus (7441)						
Section 157						
(7489)	7489	7500	7510	7520		7536
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7489)	TTTTGCAAGCTTCCAACAGGGATGTATCCTGTATCATTCATTAAACAT					
Consensus (7489)						
Section 158						
(7537)	7537	7550	7560	7570		7584
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7537)	AGTTTAAAGGCTATCACTAATGCATGTTAATATTGCCTATGCTGCTCT					
Consensus (7537)						
Section 159						
(7585)	7585	7590	7600	7610	7620	7632
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7585)	ATTTTACTCAATCCATTCTTCACAAGTCTTGGTTAAAGAATGTCACAT					
Consensus (7585)						
Section 160						
(7633)	7633	7640	7650	7660	7670	7680
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7633)	ATTGGTGATAGAATGAATTCAACCTGCTCTGTCCATTATGTCAAGCAG					
Consensus (7633)						
Section 161						
(7681)	7681	7690	7700	7710		7728
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7681)	AATAATTTGAAGCTATTTACAAACACCTTTACTTTTGCACTTTTAATT					
Consensus (7681)						

Section 162						
(7729)	7729	7740	7750	7760	7776	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7729)	CAACATGAGTATCATATGGTATCTCTCTGGATTTC	AAGGAAACACACT				
Consensus (7729)						
Section 163						
(7777)	7777	7790	7800	7810	7824	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7777)	GGATACTGCCTACTGACAAAACCTATTCTTCATATTTGCTAAAAATA					
Consensus (7777)						
Section 164						
(7825)	7825	7830	7840	7850	7860	7872
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7825)	TGTCTAAAACCTTGTTTAAATATAAATAATGTAAAAATATAATCAACTT					
Consensus (7825)						
Section 165						
(7873)	7873	7880	7890	7900	7910	7920
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (7873)	TATTTGTCAGCATTTTGTACATAAGAAAATTATTTTCAGGTTGATGAC					
Consensus (7873)						
Section 166						
(7921)	7921	7930	7940	7950	7968	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7921)	ATCACAATTTATTTTACTTTATGCTTTTGCTTTTGATTTTAAATCACA					
Consensus (7921)						
Section 167						
(7969)	7969	7980	7990	8000	8016	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (7969)	ATTCCAAACTTTTGAATCCATAAGATTTTTC	AATGGATAATTTCTTAA				
Consensus (7969)						
Section 168						
(8017)	8017	8030	8040	8050	8064	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (8017)	AATAAAAGTTAGATAATGGGTTTTATGGATTTCTTTGTTATAATATAT					
Consensus (8017)						

Section 169							
	(8065)	8065	8070	8080	8090	8100	8112
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	-----
JeongAF225987 (8065)		TTTCTACCATTCCAATAGGAGATACATTGGTCAAACACTCAAACCTAG					
Consensus (8065)		-----	-----	-----	-----	-----	-----
Section 170							
	(8113)	8113	8120	8130	8140	8150	8160
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	-----
JeongAF225987 (8113)		ATCATTTTCTACCAACTATGGTTGCCTCAATATAACCTTTTATTCATA					
Consensus (8113)		-----	-----	-----	-----	-----	-----
Section 171							
	(8161)	8161	8170	8180	8190	8208	
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	
JeongAF225987 (8161)		GATGTTTTTTTTTATTCAACTTTTGTAGTATTTACGTATGCAGACTAG					
Consensus (8161)		-----	-----	-----	-----	-----	
Section 172							
	(8209)	8209	8220	8230	8240	8256	
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	
JeongAF225987 (8209)		TCTTATTTTTTTTAATTCCTGCTGCACTAAAGCTATTACAAATATAACA					
Consensus (8209)		-----	-----	-----	-----	-----	
Section 173							
	(8257)	8257	8270	8280	8290	8304	
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	
JeongAF225987 (8257)		TGGACTTTGTTCTTTTGTAGCCATGAACAAAGTGGCAAAGTTGTGCAAT					
Consensus (8257)		-----	-----	-----	-----	-----	
Section 174							
	(8305)	8305	8310	8320	8330	8340	8352
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	-----
JeongAF225987 (8305)		TACCTAACATGATATAAATTTTGTGTTTTTGCACAAACCAAAGTTTA					
Consensus (8305)		-----	-----	-----	-----	-----	-----
Section 175							
	(8353)	8353	8360	8370	8380	8390	8400
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)		-----	-----	-----	-----	-----	-----
JeongAF225987 (8353)		ATGTTAATTCCTTTTACAAACTATTTACTGTAGTGTATTGAAGAACT					
Consensus (8353)		-----	-----	-----	-----	-----	-----

Section 176						
	(8401)	8401	8410	8420	8430	8448
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8401)	GCATGCAGGGAATTGCTATTGCTAAAAAGAATGGTGAGCTACGTCATT				
Consensus	(8401)					
Section 177						
	(8449)	8449	8460	8470	8480	8496
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8449)	ATTGAGCCAAAAGAATAAATTTTCATTTTTTTATTGCATTTCACTTATTG				
Consensus	(8449)					
Section 178						
	(8497)	8497	8510	8520	8530	8544
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8497)	GGCTCTGGGGTTTTTTGTTTTTGTGTTTTTGCTGTTGGCAGTTTAAAT				
Consensus	(8497)					
Section 179						
	(8545)	8545	8550	8560	8570	8592
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8545)	ATATATAATTAATAAAACCTGTGCTTGATCTGACATTTGTATACATAA				
Consensus	(8545)					
Section 180						
	(8593)	8593	8600	8610	8620	8640
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8593)	AAGTTTACATGAATTTTACAACAACTAGTGCATGATTCACCAAGCAG				
Consensus	(8593)					
Section 181						
	(8641)	8641	8650	8660	8670	8688
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8641)	TACTACAGAACAAAGGCAAATTAAAAGCAGCTTTGTGAACTTTTATGT				
Consensus	(8641)					
Section 182						
	(8689)	8689	8700	8710	8720	8736
ClareAJ251507	(6600)	-----				
huNall18 (AK)	(6090)	-----				
JeongAF225987	(8689)	GTGCAAAGGATCAAGTTCACATGTTCCAACCTTCAGGTTTGATAATAA				
Consensus	(8689)					

Section 183						
(8737)	8737	8750	8760	8770	8784	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (8737)	TAGTAGTAACCACCTACAATAGCTTTCAATTTCAATTAACTCCCTTGG					
Consensus (8737)						
Section 184						
(8785)	8785	8790	8800	8810	8820	8832
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (8785)	CTATAAGCATCTAAACTCATCTTCTTTCAATATAATTGATGCTATCTC					
Consensus (8785)						
Section 185						
(8833)	8833	8840	8850	8860	8870	8880
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (8833)	CTAATTACTTGGTGGCTAATAAATGTTACATTCTTTGTTACTTAAATG					
Consensus (8833)						
Section 186						
(8881)	8881	8890	8900	8910	8928	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (8881)	CATTATATAAACTCCTATGTATACATAAGGTATTAATGATATAGTTAT					
Consensus (8881)						
Section 187						
(8929)	8929	8940	8950	8960	8976	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (8929)	TGAGAATTTATATTAACCTTTTTTTTCAAGAACCCTTGGATTTATGTGA					
Consensus (8929)						
Section 188						
(8977)	8977	8990	9000	9010	9024	
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	
JeongAF225987 (8977)	GGTCAAACCAAACCTCTTATTCTCAGTGGAAACCTCCAGTTGTAATGC					
Consensus (8977)						
Section 189						
(9025)	9025	9030	9040	9050	9060	9072
ClareAJ251507 (6600)	-----	-----	-----	-----	-----	-----
huNall18 (AK) (6090)	-----	-----	-----	-----	-----	-----
JeongAF225987 (9025)	ATATTTTTTAAAGACAATTTGGATCTAAATATGTATTTTCATAATTCTCC					
Consensus (9025)						

Section 190

	(9073)	9073	9080	9090	9100	9110	9120
ClareAJ251507 (6600)		-----	-----	-----	-----	-----	-----
huNaIII18 (AK) (6090)		-----	-----	-----	-----	-----	-----
JeongAF225987 (9073)		CATAATAAATTATATAAGGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA					
Consensus (9073)							

Section 191

	(9121)	9123
ClareAJ251507 (6600)		---
huNaIII18 (AK) (6090)		---
JeongAF225987 (9121)		AAA
Consensus (9121)		

		Section 1					
		(1)	1	10	20	30	40
ClareAJ251507protein		(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKE				
Translation of huNall18 (AK)		(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKE				
Translation of JeongAF225987		(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKE				
Consensus		(1)	MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKE				
		Section 2					
		(41)	41	50	60	70	80
ClareAJ251507protein		(41)	QDNDDENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPLEDL				
Translation of huNall18 (AK)		(41)	QDNDDENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPLEDL				
Translation of JeongAF225987		(41)	QDNDDENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPLEDL				
Consensus		(41)	QDNDDENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPLEDL				
		Section 3					
		(81)	81	90	100	110	120
ClareAJ251507protein		(81)	DPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKI				
Translation of huNall18 (AK)		(81)	DPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKI				
Translation of JeongAF225987		(81)	DPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKI				
Consensus		(81)	DPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKI				
		Section 4					
		(121)	121	130	140	150	160
ClareAJ251507protein		(121)	AIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYT				
Translation of huNall18 (AK)		(121)	AIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYT				
Translation of JeongAF225987		(121)	AIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYT				
Consensus		(121)	AIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYT				
		Section 5					
		(161)	161	170	180	190	200
ClareAJ251507protein		(161)	FTGIYTFESLIKILARGFCLEDFTFLRDPWNWLD FSVIVM				
Translation of huNall18 (AK)		(161)	FTGIYTFESLIKILARGFCLEDFTFLRDPWNWLD FSVIVM				
Translation of JeongAF225987		(161)	FTGIYTFESLIKILARGFCLEDFTFLRDPWNWLD FSVIVM				
Consensus		(161)	FTGIYTFESLIKILARGFCLEDFTFLRDPWNWLD FSVIVM				
		Section 6					
		(201)	201	210	220	230	240
ClareAJ251507protein		(201)	AYVTEFVSLGNVSALRTFRVLRA LKTISVIPGLKTIVGAL				
Translation of huNall18 (AK)		(201)	AYVTEFVSLGNVSALRTFRVLRA LKTISVIPGLKTIVGAL				
Translation of JeongAF225987		(201)	AYVTEFVDLGNVSALRTFRVLRA LKTISVIPGLKTIVGAL				
Consensus		(201)	AYVTEFVSLGNVSALRTFRVLRA LKTISVIPGLKTIVGAL				
		Section 7					
		(241)	241	250	260	270	280
ClareAJ251507protein		(241)	IQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLRNKCLQW				
Translation of huNall18 (AK)		(241)	IQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLRNKCLQW				
Translation of JeongAF225987		(241)	IQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLRNKCLQW				
Consensus		(241)	IQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLRNKCLQW				

Section 8

	(281)	281	290	300	310	320
ClareAJ251507protein	(281)	PPSDSAFETNTT	SYFNGTMDSNGT	FVNVTMSTF	NWKDYIG	
Translation of huNaIII18 (AK)	(281)	PPSDSAFETNTT	SYFNGTMDSNGT	FVNVTMSTF	NWKDYIG	
Translation of JeongAF225987	(281)	PPSDSAFETNTT	SYFNGTMDSNGT	FVNVTMSTF	NWKDYIG	
Consensus	(281)	PPSDSAFETNTT	SYFNGTMDSNGT	FVNVTMSTF	NWKDYIG	

Section 9

	(321)	321	330	340	350	360
ClareAJ251507protein	(321)	DDSHFYVLDGQK	DPLLCGNGSDAG	QCPEGYICVK	AGRNP	
Translation of huNaIII18 (AK)	(321)	DDSHFYVLDGQK	DPLLCGNGSDAG	QCPEGYICVK	AGRNP	
Translation of JeongAF225987	(321)	DDSHFYVLDGQK	DPLLCGNGSDAG	QCPEGYICVK	AGRNP	
Consensus	(321)	DDSHFYVLDGQK	DPLLCGNGSDAG	QCPEGYICVK	AGRNP	

Section 10

	(361)	361	370	380	390	400
ClareAJ251507protein	(361)	YGYTSFDTFSWA	FLSLFRMTQDY	WENLYQLTLRA	AGKTY	
Translation of huNaIII18 (AK)	(361)	YGYTSFDTFSWA	FLSLFRMTQDY	WENLYQLTLRA	AGKTY	
Translation of JeongAF225987	(361)	YGYTSFDTFSWA	FLSLFRMTQDY	WENLYQLTLRA	AGKTY	
Consensus	(361)	YGYTSFDTFSWA	FLSLFRMTQDY	WENLYQLTLRA	AGKTY	

Section 11

	(401)	401	410	420	430	440
ClareAJ251507protein	(401)	MIFFVLVIFLGS	FYLVNLILAVVA	MAYEEQNQATL	EEAEQ	
Translation of huNaIII18 (AK)	(401)	MIFFVLVIFLGS	FYLVNLILAVVA	MAYEEQNQATL	EEAEQ	
Translation of JeongAF225987	(401)	MIFFVLVIFLGS	FYLVNLILAVVA	MAYEEQNQATL	EEAEQ	
Consensus	(401)	MIFFVLVIFLGS	FYLVNLILAVVA	MAYEEQNQATL	EEAEQ	

Section 12

	(441)	441	450	460	470	480
ClareAJ251507protein	(441)	KEAEFQQMLEQL	KKQQEEAQAVAA	ASAASRDFSGI	GGLGE	
Translation of huNaIII18 (AK)	(441)	KEAEFQQMLEQL	KKQQEEAQAVAA	ASAASRDFSGI	GGLGE	
Translation of JeongAF225987	(441)	KEAEFQQMLEQL	KKQQEEAQAVAA	ASAASRDFSGI	GGLGE	
Consensus	(441)	KEAEFQQMLEQL	KKQQEEAQAVAA	ASAASRDFSGI	GGLGE	

Section 13

	(481)	481	490	500	510	520
ClareAJ251507protein	(481)	LLESSEASKLSSK	SAKEWRNRKRR	QREHLEGNNK	GER	
Translation of huNaIII18 (AK)	(481)	LLESSEASKLSSK	SAKEWRNRKRR	QREHLEGNNK	GER	
Translation of JeongAF225987	(481)	LLESSEASKLSSK	SAKEWRNRKRR	QREHLEGNNK	GER	
Consensus	(481)	LLESSEASKLSSK	SAKEWRNRKRR	QREHLEGNNK	GER	

Section 14

	(521)	521	530	540	550	560
ClareAJ251507protein	(521)	DSFPKSESEDSV	KRSSFLFSMDGN	NRLTSDKKFC	SPHQSL	
Translation of huNaIII18 (AK)	(521)	DSFPKSESEDSV	KRSSFLFSMDGN	NRLTSDKKFC	SPHQSL	
Translation of JeongAF225987	(521)	DSFPKSESEDSV	KRSSFLFSMDGN	NRLTSDKKFC	SPHQSL	
Consensus	(521)	DSFPKSESEDSV	KRSSFLFSMDGN	NRLTSDKKFC	SPHQSL	

						Section 15
	(561)	561	570	580	590	600
ClareAJ251507protein	(561)	SIRGSLFSPRRNSKTSIFSFRGRAKDVGSSENFADDEHST				
Translation of huNall18 (AK)	(561)	SIRGSLFSPRRNSKTSIFSFRGRAKDVGSSENFADDEHST				
Translation of JeongAF225987	(561)	SIRGSLFSPRRNSKTSIFSFRGRAKDVGSSENFADDEHST				
Consensus	(561)	SIRGSLFSPRRNSKTSIFSFRGRAKDVGSSENFADDEHST				
						Section 16
	(601)	601	610	620	630	640
ClareAJ251507protein	(601)	FEDSESRRDSLFPVPHRHGERRNS-----				
Translation of huNall18 (AK)	(601)	FEDSESRRDSLFPVPHRHGERRNSNVSQASMSSRMVPGPLPA				
Translation of JeongAF225987	(601)	FEDGESRRDSLFPVPHRHGERRNSNVSQASMSSRMVPGPLPA				
Consensus	(601)	FEDSESRRDSLFPVPHRHGERRNSNVSQASMSSRMVPGPLPA				
						Section 17
	(641)	641	650	660	670	680
ClareAJ251507protein	(624)	-----NGTTTETE				
Translation of huNall18 (AK)	(641)	NGKMHSTVDCNGVVS LVGGPSALT SPTGQLPPEGTTTETE				
Translation of JeongAF225987	(641)	NGKMHSTVDCNGVVS LVGGPSALT SPTGQLPPEGTTTETE				
Consensus	(641)	NGKMHSTVDCNGVVS LVGGPSALT SPTGQLPPEGTTTETE				
						Section 18
	(681)	681	690	700	710	720
ClareAJ251507protein	(632)	VRKRR LSSYQISM EML EDSSGRQRAVSIASILTNTMEELE				
Translation of huNall18 (AK)	(681)	VRKRR LSSYQISM EML EDSSGRQRAVSIASILTNTMEELE				
Translation of JeongAF225987	(681)	VRKRR LSSYQISM EML EDSSGRQRAVSIASILTNTMEELE				
Consensus	(681)	VRKRR LSSYQISM EML EDSSGRQRAVSIASILTNTMEELE				
						Section 19
	(721)	721	730	740	750	760
ClareAJ251507protein	(672)	ESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDP				
Translation of huNall18 (AK)	(721)	ESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDP				
Translation of JeongAF225987	(721)	ESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDP				
Consensus	(721)	ESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDP				
						Section 20
	(761)	761	770	780	790	800
ClareAJ251507protein	(712)	FVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT				
Translation of huNall18 (AK)	(761)	FVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT				
Translation of JeongAF225987	(761)	FVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT				
Consensus	(761)	FVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT				
						Section 21
	(801)	801	810	820	830	840
ClareAJ251507protein	(752)	GIFTAEMVLKIIAMDPY YFFQEGWNIFDGIIVSLSLMELG				
Translation of huNall18 (AK)	(801)	GIFTAEMVLKIIAMDPY YFFQEGWNIFDGIIVSLSLMELG				
Translation of JeongAF225987	(801)	GIFTAEMVLKIIAMDPY YFFQEGWNIFDGIIVSLSLMELG				
Consensus	(801)	GIFTAEMVLKIIAMDPY YFFQEGWNIFDGIIVSLSLMELG				

Section 22

	(841)	841	850	860	870	880
ClareAJ251507protein	(792)	LSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVG				
Translation of huNall18 (AK)	(841)	LSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVG				
Translation of JeongAF225987	(841)	LSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVG				
Consensus	(841)	LSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVG				

Section 23

	(881)	881	890	900	910	920
ClareAJ251507protein	(832)	ALGNLTlVLAIIVFIFAVVGMQLFGKSYKECVCKINDDET				
Translation of huNall18 (AK)	(881)	ALGNLTlVLAIIVFIFAVVGMQLFGKSYKECVCKINDDET				
Translation of JeongAF225987	(881)	ALGNLTlVLAIIVFIFAVVGMQLFGKSYKECVCKINDDET				
Consensus	(881)	ALGNLTlVLAIIVFIFAVVGMQLFGKSYKECVCKINDDET				

Section 24

	(921)	921	930	940	950	960
ClareAJ251507protein	(872)	LPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCT				
Translation of huNall18 (AK)	(921)	LPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCT				
Translation of JeongAF225987	(921)	LPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCT				
Consensus	(921)	LPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCT				

Section 25

	(961)	961	970	980	990	1000
ClareAJ251507protein	(912)	LIVFMLVMVIGNLVVLNLFLLALLSSFSSDNLAATDDDDNE				
Translation of huNall18 (AK)	(961)	LIVFMLVMVIGNLVVLNLFLLALLSSFSSDNLAATDDDDNE				
Translation of JeongAF225987	(961)	LIVFMLVMVIGNLVVLNLFLLALLSSFSSDNLAATDDDDNE				
Consensus	(961)	LIVFMLVMVIGNLVVLNLFLLALLSSFSSDNLAATDDDDNE				

Section 26

	(1001)	1001	1010	1020	1030	1040
ClareAJ251507protein	(952)	MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIH				
Translation of huNall18 (AK)	(1001)	MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIH				
Translation of JeongAF225987	(1001)	MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIH				
Consensus	(1001)	MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIH				

Section 27

	(1041)	1041	1050	1060	1070	1080
ClareAJ251507protein	(992)	EGNKIDSCMSNNTGIEISKELNYLRDNGGTTSGVGTGSSV				
Translation of huNall18 (AK)	(1041)	EGNKIDSCMSNNTGIEISKELNYLRDNGGTTSGVGTGSSV				
Translation of JeongAF225987	(1041)	EGNKIDSCMSNNTGIEISKELNYLRDNGGTTSGVGTGSSV				
Consensus	(1041)	EGNKIDSCMSNNTGIEISKELNYLRDNGGTTSGVGTGSSV				

Section 28

	(1081)	1081	1090	1100	1110	1120
ClareAJ251507protein	(1032)	EKYVIDENDYMSFINNPSLTVTVPPIAVGESDFENLNTEEF				
Translation of huNall18 (AK)	(1081)	EKYVIDENDYMSFINNPSLTVTVPPIAVGESDFENLNTEEF				
Translation of JeongAF225987	(1081)	EKYVIDENDYMSFINNPSLTVTVPPIAVGESDFENLNTEEF				
Consensus	(1081)	EKYVIDENDYMSFINNPSLTVTVPPIAVGESDFENLNTEEF				

Section 29

	(1121)	1121	1130	1140	1150	1160
ClareAJ251507protein (1072)		SSESELEESKEKLNATSSSEGSTVDVVL	PREGEQAETEPE			
Translation of huNall18 (AK) (1121)		SSESELEESKEKLNATSSSEGSTVDVVL	PREGEQAETEPE			
Translation of JeongAF225987 (1121)		SSESELEESKEKLNATSSSEGSTVDVVL	PREGEQAETEPE			
Consensus (1121)		SSESELEESKEKLNATSSSEGSTVDVVL	PREGEQAETEPE			

Section 30

	(1161)	1161	1170	1180	1190	1200
ClareAJ251507protein (1112)		EDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL	RKTCY			
Translation of huNall18 (AK) (1161)		EDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL	RKTCY			
Translation of JeongAF225987 (1161)		EDFKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL	RKTCY			
Consensus (1161)		EDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNL	RKTCY			

Section 31

	(1201)	1201	1210	1220	1230	1240
ClareAJ251507protein (1152)		SIVEHWNFETFIVFMILLSSGALAFEDIYIEQRKTIKTML				
Translation of huNall18 (AK) (1201)		SIVEHWNFETFIVFMILLSSGALAFEDIYIEQRKTIKTML				
Translation of JeongAF225987 (1201)		SIVEHWNFETFIVFMILLSSGALAFEDIYIEQRKTIKTML				
Consensus (1201)		SIVEHWNFETFIVFMILLSSGALAFEDIYIEQRKTIKTML				

Section 32

	(1241)	1241	1250	1260	1270	1280
ClareAJ251507protein (1192)		EYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLD	FLIV			
Translation of huNall18 (AK) (1241)		EYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLD	FLIV			
Translation of JeongAF225987 (1241)		EYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLD	FLIV			
Consensus (1241)		EYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLD	FLIV			

Section 33

	(1281)	1281	1290	1300	1310	1320
ClareAJ251507protein (1232)		DVSLVSLVANALGYSELGAIKSLRTLRLRPLRLSRFEG				
Translation of huNall18 (AK) (1281)		DVSLVSLVANALGYSELGAIKSLRTLRLRPLRLSRFEG				
Translation of JeongAF225987 (1281)		DVSLVSLVANALGYSELGAIKSLRTLRLRPLRLSRFEG				
Consensus (1281)		DVSLVSLVANALGYSELGAIKSLRTLRLRPLRLSRFEG				

Section 34

	(1321)	1321	1330	1340	1350	1360
ClareAJ251507protein (1272)		MRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNL	FAKG			
Translation of huNall18 (AK) (1321)		MRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNL	FAKG			
Translation of JeongAF225987 (1321)		MRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNL	FAKG			
Consensus (1321)		MRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNL	FAKG			

Section 35

	(1361)	1361	1370	1380	1390	1400
ClareAJ251507protein (1312)		FYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNV	KVNF			
Translation of huNall18 (AK) (1361)		FYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNV	KVNF			
Translation of JeongAF225987 (1361)		FYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNV	KVNF			
Consensus (1361)		FYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNV	KVNF			

Section 36

	(1401)	1401	1410	1420	1430	1440
ClareAJ251507protein (1352)		DNVGAGYLALLQVAT	FKGWMDIMYAAVDS	RDVKLQPVYEE		
Translation of huNall18 (AK) (1401)		DNVGAGYLALLQVAT	FKGWMDIMYAAVDS	RDVKLQPVYEE		
Translation of JeongAF225987 (1401)		DNVGAGYLALLQVAT	FKGWMDIMYAAVDS	RDVKLQPVYEE		
Consensus (1401)		DNVGAGYLALLQVAT	FKGWMDIMYAAVDS	RDVKLQPVYEE		

Section 37

	(1441)	1441	1450	1460	1470	1480
ClareAJ251507protein (1392)		NLYMYLYFVIFII	FGSFFTLNLF	FIGVIIDNFN	QQKKKFGG	
Translation of huNall18 (AK) (1441)		NLYMYLYFVIFII	FGSFFTLNLF	FIGVIIDNFN	QQKKKFGG	
Translation of JeongAF225987 (1441)		NLYMYLYFVIFII	FGSFFTLNLF	FIGVIIDNFN	QQKKKFGG	
Consensus (1441)		NLYMYLYFVIFII	FGSFFTLNLF	FIGVIIDNFN	QQKKKFGG	

Section 38

	(1481)	1481	1490	1500	1510	1520
ClareAJ251507protein (1432)		QDIFMTEEQKKY	NAMKKLGSKK	PKPIPRPANK	FQGMVF	
Translation of huNall18 (AK) (1481)		QDIFMTEEQKKY	NAMKKLGSKK	PKPIPRPANK	FQGMVF	
Translation of JeongAF225987 (1481)		QDIFMTEEQKKY	NAMKKLGSKK	PKPIPRPANK	FQGMVF	
Consensus (1481)		QDIFMTEEQKKY	NAMKKLGSKK	PKPIPRPANK	FQGMVF	

Section 39

	(1521)	1521	1530	1540	1550	1560
ClareAJ251507protein (1472)		DFVTRQVFDIS	SIMILICLNM	VMTMMVETDD	QGKYMTLVLSR	
Translation of huNall18 (AK) (1521)		DFVTRQVFDIS	SIMILICLNM	VMTMMVETDD	QGKYMTLVLSR	
Translation of JeongAF225987 (1521)		DFVTRQVFDIS	SIMILICLNM	VMTMMVETDD	QGKYMTLVLSR	
Consensus (1521)		DFVTRQVFDIS	SIMILICLNM	VMTMMVETDD	QGKYMTLVLSR	

Section 40

	(1561)	1561	1570	1580	1590	1600
ClareAJ251507protein (1512)		INLVFIVLFTGE	FVLKLVSLRH	YYFTIGWNIF	DFVNVILS	
Translation of huNall18 (AK) (1561)		INLVFIVLFTGE	FVLKLVSLRH	YYFTIGWNIF	DFVNVILS	
Translation of JeongAF225987 (1561)		INLVFIVLFTGE	FVLKLVSLRH	YYFTIGWNIF	DFVNVILS	
Consensus (1561)		INLVFIVLFTGE	FVLKLVSLRH	YYFTIGWNIF	DFVNVILS	

Section 41

	(1601)	1601	1610	1620	1630	1640
ClareAJ251507protein (1552)		IVGMFLAEMIEK	YFVSPTLFR	VIRLARIGRIL	RRLIKGAKG	
Translation of huNall18 (AK) (1601)		IVGMFLAEMIEK	YFVSPTLFR	VIRLARIGRIL	RRLIKGAKG	
Translation of JeongAF225987 (1601)		IVGMFLAEMIEK	YFVSPTLFR	VIRLARIGRIL	RRLIKGAKG	
Consensus (1601)		IVGMFLAEMIEK	YFVSPTLFR	VIRLARIGRIL	RRLIKGAKG	

Section 42

	(1641)	1641	1650	1660	1670	1680
ClareAJ251507protein (1592)		IRTLLFALMMSLP	ALFNIGLLL	FLVMFIYAIF	GMSNFAYV	
Translation of huNall18 (AK) (1641)		IRTLLFALMMSLP	ALFNIGLLL	FLVMFIYAIF	GMSNFAYV	
Translation of JeongAF225987 (1641)		IRTLLFALMMSLP	ALFNIGLLL	FLVMFIYAIF	GMSNFAYV	
Consensus (1641)		IRTLLFALMMSLP	ALFNIGLLL	FLVMFIYAIF	GMSNFAYV	

Section 43

	(1681)	1681	1690	1700	1710	1720
ClareAJ251507protein (1632)		KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILN				
Translation of huNall18 (AK) (1681)		KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILN				
Translation of JeongAF225987 (1681)		KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILN				
Consensus (1681)		KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILN				

Section 44

	(1721)	1721	1730	1740	1750	1760
ClareAJ251507protein (1672)		SAPPDCDPDTIHPGSSVKGDCGNPSVGIFFFVSYIIISFL				
Translation of huNall18 (AK) (1721)		SAPPDCDPDTIHPGSSVKGDCGNPSVGIFFFVSYIIISFL				
Translation of JeongAF225987 (1721)		SAPPDCDPDTIHPGSSVKGDRGDPVGIFFFVSYIIISFL				
Consensus (1721)		SAPPDCDPDTIHPGSSVKGDCGNPSVGIFFFVSYIIISFL				

Section 45

	(1761)	1761	1770	1780	1790	1800
ClareAJ251507protein (1712)		VVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWEKF				
Translation of huNall18 (AK) (1761)		VVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWEKF				
Translation of JeongAF225987 (1761)		VVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWEKF				
Consensus (1761)		VVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWEKF				

Section 46

	(1801)	1801	1810	1820	1830	1840
ClareAJ251507protein (1752)		DPDATQFIEFSKLSDFAAALDPPLLIAPKNKVQLIAMDL P				
Translation of huNall18 (AK) (1801)		DPDATQFIEFSKLSDFAAALDPPLLIAPKNKVQLIAMDL P				
Translation of JeongAF225987 (1801)		DPDATQFIEFSKLSDFAAALDPPLLIAPKNKVQLIAMDL P				
Consensus (1801)		DPDATQFIEFSKLSDFAAALDPPLLIAPKNKVQLIAMDL P				

Section 47

	(1841)	1841	1850	1860	1870	1880
ClareAJ251507protein (1792)		MVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEDRFMA				
Translation of huNall18 (AK) (1841)		MVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEDRFMA				
Translation of JeongAF225987 (1841)		MVSGDRIHCLDILFAFTKRVLCEGEMDALRIQMEDRFMA				
Consensus (1841)		MVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEDRFMA				

Section 48

	(1881)	1881	1890	1900	1910	1920
ClareAJ251507protein (1832)		SNPSKVSYPEPITTTTLKRKQEEVSAAI IQRNFRCYLLKQRL				
Translation of huNall18 (AK) (1881)		SNPSKVSYPEPITTTTLKRKQEEVSAAI IQRNFRCYLLKQRL				
Translation of JeongAF225987 (1881)		SNPSKVSYPEPITTTTLKRKQEEVSAAI IQRNFRCYLLKQRL				
Consensus (1881)		SNPSKVSYPEPITTTTLKRKQEEVSAAI IQRNFRCYLLKQRL				

Section 49

	(1921)	1921	1930	1940	1950	1960
ClareAJ251507protein (1872)		KNISSNYNKEAIKGRIDLPIKQDMIIDKLN GNSTPEKTDG				
Translation of huNall18 (AK) (1921)		KNISSNYNKEAIKGRIDLPIKQDMIIDKLN GNSTPEKTDG				
Translation of JeongAF225987 (1921)		KNISSNYNKEAIKGRIDLPIKQDMIIDKLN GNSTPEKTDG				
Consensus (1921)		KNISSNYNKEAIKGRIDLPIKQDMIIDKLN GNSTPEKTDG				

Section 50

	(1961)	1961	1970	1980	1990	2000
ClareAJ251507protein (1912)	SSSTT	\$	PPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK			
Translation of huNall118 (AK) (1961)	SSSTT	\$	PPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK			
Translation of JeongAF225987 (1961)	SSSTT	PPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK				
Consensus (1961)	SSSTT	PPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK				

Figure 3

